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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 May 16, 2003, 10:12:16; Search time
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseq/geneseqp-jembl/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-jembl/AA1982.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-jembl/AA1983.DAT:*
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                                                                                       /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
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167.515 Million cell updates/sec
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to have a being printed,
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Pred. No. is the number of results predicted by chance to score greater than or equal to the score of the result being and is derived by analysis of the total score distribution

## SUMMARIES

10987654321	Result
179 179 179 179 176 174 174 174 174	Score
	Query Match 1
419 419 419 419 419 419	Length DB
2222222222	₩
AAY18300 AAE08630 AAB82677 AAB82677 AAW18301 AAE08627 AAE08628 AAE08628 AAB82675 AAB82676	ID
Modified GLA domai Human protein C de Human protein C de Human protein C de Muman protein C de Human protein C de	Description

	11111111111111111111111111111111111111	
	173 1170 1168 1168 1160 1160 1160 1160 1160 116	
	888888888888888888888888888888888888888	
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ALIGNMENTS	AAY18298 AAY18299 AAY18307 AAY18309 AAY18309 AAY18303 AAK1836402 AAW756803 AAK756803 A	
	Modified G Modified G Modified G Modified G Modified G Modified G Human prott Human prott Human prott Human matu Wild-type Human prott	
	GLA CGLA CGLA CGLA CGLA CGLA CGLA CGLA C	
	NA A A A A A A A A A A A A A A A A A A	

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RESULT 1
AAY18300
ID AAY18300 standard; peptide; 44 AA.

XX
AC AAY18300;
XX
DT 17-AUG-1999 (first entry)
XX
DE Modified GLA domain of vitamin K-depend
XX
C GLA domain; mutein; vitamin K-depend
XX
C Synthetic:
XX
C Synthetic:
XX
PH Key Location/Qualifiers
FT Misc-difference 1..44
FT Misc-difference 1..44
FT Wisc-difference 1..47
FT Wisc-difference 1..48
FT Wisc-difference 1..49
FT Wisc-difference 1..49
FT Wisc-difference 1..40
FT Wisc-difference 1..41
FT Wisc-difference 1..42
FT Wisc-difference 1..43
FT Wisc-difference 1..44
FT Wisc-differen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified GLA domain of vitamin K-dependent protein.
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acid"
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RESULT 2
AAE08630
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Best Local S
Matches 44
       The invention relates to human protein C derivatives and nucleic acid molecules encoding such derivatives. These derivatives have increased anticoagulation activity, resistance to serpin inactivation and
                                                                                       Protein C derivative for treating acute coronary syndromes, vasocclusive disorders, thrombotic disorders and sepsis, comprises substitutions at specified amino acid positions
                                                                  Claim 6;
                                                                                                                                                                                                Gerlitz
                                                                                                                                                                                                                                                                                                                                                                                                 vascular occlusive disorder; hypercoagulable state; angina; sepsis; disseminated intravascular coagulation; DIC, burn; transplantation; sickle cell disease; viral haemorrhagic fever; protein C deficiency; haemolytic uremic syndrome; acute arterial thrombotic occlusion; thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.
                                                                                                                                                                                                                        (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                    11-FEB-2000;
14-MAR-2000;
                                                                                                                                                                                                                                                                                             02-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; protein C der serpin inactivation;
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                                                                                                                                                                 2001-514662/56
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                                                                                                                                                                                              BE,
                                                                    Page 50-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44
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2000US-0189199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C derivative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           derivative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide with modified for treating clotting disc
                                                                59pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ivative; anticoagulation activity; thrombosis;
acute coronary syndrome; myocardial infarctio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.9%;
                                                                                                                                                                                              BW,
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          myocardial infarction;
state; angina; sepsis;
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Best Local
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                                                                                                                Disulfide-bond
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                                                                                                                                         Disulfide-bond
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                                                                                                                                                                               Domain
                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                          myocardial infarction; sepsis; protein C deficiency; occlusion; hypercoagulation; sepsis; protein C deficiency; occlusion; thromboembolism; stenosis; antibacterial; immunosuppressive; thromboembolism; stenosis; antibacterial; anticoagulant; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 permeability increasing protein; thrombotic disorders in combination with an anti-platelet agent; protein C deficiency; acute arterial thrombotic occlusion, thromboembolism or stenosis in coronary, cerebral or peripheral arteries or in vascular grafts in combination with a thrombolytic agent. Nucleic acid molecules of the invention are useful for treating humans with genetically predisposed prothrombotic disorders
                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                   mutant; mutein
                                                                                                                                                                                                                                                                                                                                                                                                                                    myocardial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB82677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB82677 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disseminated intravascular coagulation (DIC), burns, transplantations, thalassaemia, sickle cell disease, viral haemorrhagic fever and
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein C. and retains the biological activity of the wild type human protein C. Protein C derivatives are useful in the manufacture of a medicament for the treatment of acute coronary syndromes e.g. myocardial infarction and unstable angina; and disease states predisposing to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                haemolytic uremic syndrome; sepsis in combination with bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombosis; vascular occlusive disorders and hypercoagulable states e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                              .fide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein C derivative (H10Q/S11G/Q32E/N33D/L194S).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                      80..89

98..109

120..133

141..277

196..212

331..345

356..384

156..157
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32
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11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                coronary syndrome; thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence
"cleavage makes a 2-chain inactive precursor (155-amino acid light c) attached via a disulfide bond to a
                                                                                                                                                                                         "Leu
                                                                                                                                                                                                                  "Asn
                                                                                                                                                                                                                                          "Gln
                                                                                                                                                                                                                                                                     "Ser
                                                                                                                                                                                                                                                                                            "His
                                                                                                                                                                   "Gla
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Pred. No. 1
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L.4e-21;
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             chain
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in which His at position 10 of the mature wild-type protein C. sequence (see AAB82673) is substituted with Gln, Ser at position 11 with Gly, Gln at position 32 with Gly, Asn at position 33 with Asp, and Leu at position 32 with Ser. It is an example of protein C derivatives of the invention that have at least 2 amino acid substitutions, but which have increased anticoagulant activity and resistance to inactivation by serpins compared with the wild-type protein, while retaining the biological activity of the wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-FEB-2000;
14-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cleavage-site
            with tissue factor pathway inhibitor), thrombotic disorders (in combination with an anti-platelet agent or by local delivery through an intracoronary catheter), protein C deficiency, acute arterial thrombotic occlusion, thromboembolism, or stenosis in coronary,
                                                                                   vascular occlusive disorders and hypercoagulable states, sepsis combination with bactericidal permeability increasing protein or
                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Page 54-55; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          Novel human protein C derivative for treating, e infarction, unstable angina, sepsis, thrombotic arterial thrombotic occlusion, and thromboemboli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ELIL ) LILLY & CO ELI.
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cerebral or
                                                                                                                      thrombosis (e.g.
                                                                                                                                                         protein. A method of producing the derivatives using recombinant DNA methods is claimed. The protein C derivatives are useful for
                                                                                                                                                                                                                                                                                                                                     The present sequence is that of a claimed human protein C derivative
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                                                                                                                                          treating
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peripheral arteries
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                                                                                                                  myocardial infarction and unstable angina)
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myocardial infarction; vascular occlusive disorder;
hypercoagulation; sepsis; protein C deficiency; occlusion;
thromboembolism; stenosis; antibacterial; immunosuppressiv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein C derivative
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precursor (155-amino acid ligh
attached via a disulfide bond
262-amino acid heavy chain)"
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Pred. No. 1.4e-21
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                                                                                                                                                                                                       an intracoronary catheter), protein C deficiency, acute arterial thrombotic occlusion, thromboembolism, or stenosis in coronary, cerebral or peripheral arteries or in vascular grafts. Human
                                                                                                                                                                                                                                                                                                                                                                                                                              in which His at position 10 of the wild-type protein C sequence (see AAB82673) is substituted with Gln, Ser at position 11 with Gly, Gln at position 32 with Glu, Asn at position 33 with Asp, Leu at position 194 with Ser, and Thr at position 254 with Ser. It is an example of protein C derivatives of the invention that have at least 2 amino acid substitutions, but which have increased anticoagulant activity and registers of the invention that have at least 2 with substitutions, but which have increased anticoagulant activity and
                                                                                                                                        Sequence
                                                                                                                                                                          be treated
                                                                                                                                                                                          patients with genetically predisposed
                                                                                                                                                                                                                                                         with tissue factor pathway inhibitor), thrombotic disorders (in combination with an anti-platelet agent or by local delivery through
                                                                                                                                                                                                                                                                                             vascular occlusive disorders and hypercoagulable states, sepsis (in combination with bactericidal permeability increasing protein or
                                                                                                                                                                                                                                                                                                                               thrombosis (e.g. myocardial infarction and unstable angina),
                                                                                                                                                                                                                                                                                                                                                                             resistance to inactivation by serpins compared with the wild-type protein, while retaining the biological activity of the wild-type protein. A method of producing the derivatives using recombinant the compared with the derivatives using recombinant that the compared with the compared with the compared with the compared with the wild-type protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human protein C derivative for treating, e.g., myocar infarction, unstable angina, sepsis, thrombotic disorders, arterial thrombotic occlusion, and thromboembolism -
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35; Conserv
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329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "N-glycosylated" 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169..170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158..169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                    90.98;
79.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is that of a claimed human protein C derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "activation peptide;
2-chain zymogen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "thrombin cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                 The protein C derivatives are useful for
                                                                                                                                                                          (all claimed).
                                                                Score 179; DB Pred. No. 1.4e 0; Mismatches
                                                                                                                                                                                          prothrombotic
                                                                                    DB 22;
.4e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            removal
                                                                    9
                                                                                                Length 419;
44
                                44
                                                                    Indels
                                                                                                                                                                                      disorders may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          myocardial
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                                                                  Gaps
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RESULT 6
AAE08627
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AAY18301
ID AAY1
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AC
                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                               Matches
                    Human protein C derivative #1.
                                            01-NOV-2001
                                                                                                                                                                                                                                                                to the native polypeptide. The polypeptide is used to treat a clott disorder by decreasing or increasing clot formation. Modification of GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.
                                                                                                                                                                                                                                                                                                                        This sequence represents a modified GLA (gamma-carboxyglutamic domain. The invention relates to a vitamin K-dependent polypept comprising a modified GLA domain containing an amino acid subst
                                                                   AAE08627;
                                                                                          AAE08627
                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                           Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                                                      which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-288309/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nelsestuen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9920767-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLA domain; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified GLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY18301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MINU ) UNIV MINNESOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY18301 standard;
                                                                                                                                                  ۳
                                                                                                                                                               ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                 ANSFLXXLREGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                       9;
                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                     Page
                                                                                                                                                                                                                                          44
                                                                                                                                                                                               Conservative
                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain
                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                       82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0955636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-US22152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Xaa= gamma-carboxyglutamic
acid"
                                                                                                                                                                                                                                                                                                                                                                   86pp;
                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide; 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of
                                                                                                                                                                                                         89.3%;
97.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vitamin K-dependent protein; clotting disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vitamin K-dependent protein
                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                          419
                                                                                                                                                                                                         Score 176; DB 20;
Pred. No. 4.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ä
                                                                                          A
                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                    Length
                                                                                                                                                 44
                                                                                                                                                                       44
                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid,
                                                                                                                                                                                                                                                                                                                                 polypeptide
                                                                                                                                                                                                                     44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ဝ္ပ
                                                                                                                                                                                                                                                                                                                         substitution
                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glutamic
                                                                                                                                                                                                                                                                                                                                              acid)
                                                                                                                                                                                              Gaps
                                                                                                                                                                                              0;
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Human;

protein C

derivative; anticoagulation activity; thrombosis;

myocardial infarction;

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AAE08628
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                                                                                                                                                                     RESULT 7
                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               molecules encoding such derivatives. These derivatives have increased anticoagulation activity, resistance to serpin inactivation and increased sensitivity to thrombin activation compared to wild type protein C, and retains the biological activity of the wild type human protein C. Protein C derivatives are useful in the manufacture of a medicament for the treatment of acute coronary syndromes e.g. myogardial infarction and unstable angina; and disease states predisposing to thrombosis; vascular occlusive disorders and hypercoagulable states e.g. disseminated intravascular coagulation (DIC), burns, transplantations, thalassaemia, sickle cell disease, viral haemorfhagic fever and haemolytic uremic syndrome; sepsis in combination with bacterial permeability increasing protein; thrombotic disorders in combination
Human; protein C derivative; anticoagulation activity; thrombosis;
                                  Human protein C derivative
                                                                    01-NOV-2001
                                                                                                     AAE08628
                                                                                                                                    AAE08628 standard;
                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                with an anti-platelet agent; protein C deficiency; acute arterial thrombotic occlusion, thromboembolism or stenosis in comonary, ce or peripheral afteries or in vascular grafts in combination with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 46-47; 59pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  substitutions at specified amino acid positions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gerlitz BE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-FEB-2000; 2000US-0181948
14-MAR-2000; 2000US-0189199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  serpin inactivation; acute coronary syndrome; myocardial infarct vascular occlusive disorder; hypercoagulable state; angina; seps disseminated intravascular coagulation; DIC; burn; transplantati sickle cell disease; viral haemorrhagic fever; protein C deficte haemolytic uremic syndrome; acute arterial thrombotic occlusion;
                                                                                                                                                                                                                                                                                                                                                                              thrombolytic agent. Nucleic acid molecules of the invention are useful for treating humans with genetically predisposed prothrombotic disorders by gene therapy. The present sequence is human protein C derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein C derivative for treating acute coronary occlusive disorders, thrombotic disorders and sep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200159084-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thromboembolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                     -
                                                                                                                                                                                                                                                  1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens.
                                                                                                                                                                                                              ANSFLEELRHGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-514662/56
                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                     419
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grinnell
                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                     3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prothrombotic disorder; gene therapy; thalassaemia
                                                                                                                                    Protein; 419
                                                                                                                                                                                                                                                                                                   88.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human protein
                                     #2
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                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                 Score 174; DB 2
Pred. No. 1e-20;
                                                                                                                                    ₿
                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       derivatives and
                                                                                                                                                                                                                                                                                                                  22; Length 419;
                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     state; angina; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    syndromes,
                                                                                                                                                                                                                   44
                                                                                                                                                                                                                                                  44
                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transplantation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   deficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vascular
                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                     cerebral
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                   0
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Q

1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH

ANSFLEELRHGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKH

Query Match Matches Best

Local

Similarity

88.3%; 77.3%;

Score 174; DB 2 Pred. No. 1e-20;

DB 22;

Length 419;

34;

Conservative

0;

Mismatches

10;

Indels

0

Gaps

0

44 44

В

**AAE08629** RESULT 8

AAE08629 standard;

Protein;

419

A

XXEXEX DXXXX

01-NOV-2001

(first entry)

AAE08629

Human

protein C

derivative

Human; protein C derivative; anticoagulation activity; thrombosis;

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thalassaemia, sickle cell disease, viral haemorrhagic fever and haemolytic uremic syndrome; sepsis in combination with bacterial permeability increasing protein; thrombotic disorders in combinatiwith an anti-platelet agent; protein C deficiency; acute arterial thrombotic occlusion, thromboembolism or stenosis in coronary, cent or peripheral arteries or in vascular grafts in combination with a composition of the combination with a composition of the combination with a composition of the combination with a combination with
                                                                                                                                                                                                                                                                                                                                                                                                                                                              molecules encoding such derivatives. These derivatives have increased anticoagulation activity, resistance to serpin inactivation and increased sensitivity to thrombin activation compared to wild type protein C, and retains the biological activity of the wild type human protein C. Protein C derivatives are useful in the manufacture of a medicament for the treatment of acute coronary syndromes e.g. myocardial
Sequence
                                                                                                                                                                                                                                                                                                                                                            infarction and unstable angina; and disease states predisposing to thrombosis; vascular occlusive disorders and hypercoagulable states e. thrombosis; vascular occlusive disorders and hypercoagulations, burns, transplantations, disseminated intravascular coagulation (DIC), burns, transplantations, burns, transplantations, and disseminated intravascular occupants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 47-48; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein C derivative for treating acute coronary syndromes, occlusive disorders, thrombotic disorders and sepsis, comprisubstitutions at specified amino acid positions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gerlitz
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                                                                                          thrombolytic agent. Nucleic acid molecules of the invention are useful for treating humans with genetically predisposed prothrombotic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thromboembolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           haemolytic uremic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-514662/56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE,
                                                           therapy. The
   419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grinnell BW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0181948
2000US-0189199
   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prothrombotic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           syndrome; acute arterial thrombotic occl
                                                              present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        derivatives and
                                                              human protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         state; angina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myocardial infarction
state; angina; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprises
                                                                  റ
                                                                                                                                                                                                                                                                         combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   deficiency;
                                                                     derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lantation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cleic acid
                                                                                                                                                                                                      cerebral
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RESULT 9
AAB82675
ID AAB8
XX
AC AAB8
XX
DT 15-0
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                                                                                                                                                 밁
                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                disseminated intravascular coagulation (DIC), burns, transplantations, thalassaemia, sickle cell disease, viral haemorrhagic fever and haemolytic uremic syndrome; sepsis in combination with bacterial permeability increasing protein; thrombotic disorders in combination with an anti-platelet agent; protein C deficiency; acute arterial thrombotic occlusion, thromboembolism or stenosis in coronary, cerebral or peripheral arteries or in vascular grafts in combination with a thrombolytic agent. Nucleic acid molecules of the invention are useful for treating humans with genetically predisposed prothrombotic disorders by gene therapy. The present sequence is human protein C derivative.
 15-OCT-2001
                                 AAB82675;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anticoagulation activity, resistance to serpin inactivation and increased sensitivity to thrombin activation compared to wild type protein C, and retains the biological activity of the wild type human protein C. Protein C derivatives are useful in the manufacture of a medicament for the treatment of acute coronary syndromes e.g. myocardial infarction and unstable angina; and disease states predisposing to
                                                                AAB82675 standard;
                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombosis; vascular occlusive disorders and hypercoagulable states e.g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human protein C derivatives and nucleic acid molecules encoding such derivatives. These derivatives have increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     substitutions at specified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein C
occlusive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gerlitz BE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-FEB-2000;
14-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-FEB-2001; 2001WO-US01221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disseminated intravascular coagulation; DIC; burn; transplantation; sickle cell disease; viral haemorrhagic fever; protein C deficiency haemolytic uremic syndrome; acute arterial thrombotic occlusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200159084-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        serpin inactivation; acute coronary syndrome; myocar vascular occlusive disorder; hypercoagulable state;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thromboembolism;
                                                                                                                                                                1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                             ANSFLEELRHGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKH
                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 48-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  derivative for treating acute coronary syndromes, vascular disorders, thrombotic disorders and sepsis, comprises
                                                                                                                                                                                                                                                                              419
                                                                                                                                                                                                               Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0181948
2000US-0189199
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                                                                                                                                                                                                                                                                              AA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prothrombotic
                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59pp;
                                                                                                                                                                                                                             88.3%;
77.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₩,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                              419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jones BE
                                                                                                                                                                                                            Score 174; DB 2
Pred. No. 1e-20;
D; Mismatches
                                                              B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorder; gene therapy; thalassaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ders and sepsis, comprises positions
                                                                                                                                                                                                                                         22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myocardial infarction
                                                                                                                                                                                                                                          Length 419;
                                                                                                                                             44
                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            angina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        deficiency
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                                                                                                                                                                                                        Gaps
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                                                                                                        Modified-site
                                                                                                                          Modified-site
                                                                                                                                             Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein C;
myocardial
                                    WO200157193-A2
                                                                 Modified-site
                                                                                                                                                                          Peptide
                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                   Modified:site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein C; human; coronary syndrome; thrombosis; angina; myocardial infarction; vascular occlusive disorder; hypercoagulation; sepsis; protein C deficiency; occlusion; thromboembolism; stenosis; antibacterial; immunosuppressiv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -bond
                                                                                                                                                                                                                                                                                                                                                                                                    bond.
                                                                                                                                                                                                                                                                                                                                                                                                              bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C derivative (S11G/Q32E/N33D/L194S).
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32
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194
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98..109
120..133
141..277
196..212
331..345
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33
                                                                /note<del>-</del>
329
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50..69
59..64
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                                                                                             'note=
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                                                                                            "N-glycosylated
                                                                                                                "N-glycosylated
                                                      "N-glycosylated
                                                                                                                                   "thrombin cleavage site"
                                                                                                                                                   "activation peptide; removal 2-chain zymogen"
                                                                                                                                                                                 "gamma-carboxylated"
                                                                                                                                                                                                    "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Gla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Ser
                                                                                                                                                                                                                                           "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                         "cleavage makes a 2-chain inactive precursor (155-amino acid light chain attached via a disulfide bond to a 262-amino acid heavy chain)"
                                                                                                                                                                                                                        "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                   "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Asn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Gln in wild-type
                                                                                                                                                                                                                                                               "gamma-carboxylated"
                                                                                                                                                                                                                                                                                "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                       "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antianginal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anticoagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein"
                                                                                                                                                                activates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        therapy;
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19-JAN-2001; 2001WO-US00020

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AABB2676
ID AABB2676
AC AABB2
XX 15-OC
XT 15-OC
XX Prote
KW Prote
KW myocas
KW throm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                         Protein C;
myocardial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA methods is claimed. The protein C derivatives are useful for treating coronary syndromes and disease states predisposing to thrombosis (e.g. myocardial infarction and unstable angina), vascular occlusive disorders and hypercoagulable states, sepsis (in combination with bactericidal permeability increasing protein or with tissue factor pathway inhibitor), thrombotic disorders (in combination with an anti-platelet agent or by local delivery through an intracoronary catheter), protein C deficiency, acute arterial thrombotic occlusion, thromboembolism, or stenosis in coronary, cerebral or peripheral arteries or in vascular grafts, luman patients with genetically predisposed prothrombotic disorders may be treated by gene therapy (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of a claimed human protein C derivative in which Ser at amino acid position il of the mature wild-type protein C sequence (see AAB82673) is substituted with Gly, Gln at position 32 with Glu, Asn at position 33 with Asp, and Leu at position 194 with Ser. The protein is an example of protei C derivatives of the invention that have at least 2 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 substitutions, but which have increased anticoagulant activity and resistance to inactivation by serpins compared with the wild-type protein, while retaining the biological activity of the wild-type
Misc-difference 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 52-53; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-FEB-2000; 2000US-0179801.
14-MAR-2000; 2000US-0189197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arterial thrombotic occlusion, and thromboembolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gerlitz BE,
                                                                                                     Synthetic
                                                                                                                             Homo sapiens.
                                                                                                                                                                                          mucant;
                                                                                                                                                                                                                      thrombolytic;
                                                                                                                                                                                                                                                     thromboembolism;
                                                                                                                                                                                                                                                                                                                                                                                                  Human protein C derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB82676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB82676 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                  hypercoagulation; sepsis; protein C deficiency; occlusion;
thromboembolism; stenosis; antibacterial; immunosuppressiv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-496919/54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A method of producing the derivatives using recombinant
                                                                                                                                                                                                                                                                                                         infarction; vascular occlusive disorder;
                                                                                                                                                                                                                                                                                                                                    human; coronary syndrome; thrombosis; angina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                419 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                      cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.3%;
                                                                                                                                                                                                                      antianginal;
                                                                                                                                                                                                                                                                                                                                                                                                  (S11G/Q32E/N33D/L194S/T254S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             419
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Pred. No. 1e-20;
0; Mismatches
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                                                                                                                                                                                                                   anticoagulant; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
                                                                                                                                                                                                                                                  immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
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Cleavage-site
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                                                                            02-FEB-2000;
14-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                        Modified-site
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                      N-PSDB;
                               WPI;
                                                            (ELIL ) LILLY & CO ELI
                                                                                                    19-JAN-2001;
                                                                                                                    09-AUG-2001
                                                                                                                                  WO200157193-A2
                                                                                                                                                         Modified-site
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                              2001-496919/54.
                                              ВE,
                       AAH26364.
                                                                                                                                                                                                                                                                                                                                                                                                                             -bond
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                                              Jones
                                                                            2000US-0179801
2000US-0189197
                                                                                                    2001WO-US00020
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120..133
141..277
196..212
331..345
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50..69
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254
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32
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                                                                                                                                                "N-glycosylated
                                                                                                                                                                 "N-glycosylated"
                                                                                                                                                                                "N-glycosylated"
                                                                                                                                                                                               "N-glycosylated"
                                                                                                                                                                                                                              "activation peptide; 2-chain zymogen"
                                                                                                                                                                                                                                                     "gamma-carboxylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Thr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Ser
                                                                                                                                                                                                                                                                     "gamma-carboxylated"
                                                                                                                                                                                                                                                                                   "gamma-carboxylated
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                                                                                                                                                                                                                                                                                                                                                "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                "gamma-carboxylated"
                                                                                                                                                                                                              "thrombin cleavage
                                                                                                                                                                                                                                                                                                                                                                               'cleavage makes a 2-chain inactive precursor (155-amino acid light clattached via a disulfide bond to a 262-amino acid heavy chain)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein"
                                                                                                                                                                                                               site"
                                                                                                                                                                                                                                      removal activates the
                                                                                                                                                                                                                                                                                                                                                                                               chain
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Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute

arterial

thrombotic

occlusion, and thromboembolism

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RESULT 11
AAY18298
ID AAY18
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Best Local S
Matches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             substitutions, but which have increased anticoagulant activity and resistance to inactivation by serpins compared with the wild-type protein, while retaining the biological activity of the wild-type protein. A method of producing the derivatives using recombinant DNA methods is claimed. The protein C derivatives are useful for treating coronary syndromes and disease states predisposing to thrombosis (e.g. myocardial infarction and unstable angina), vascular occlusive disorders and hypercoagulable states, sepsis (in combination with bactericidal permeability increasing protein or with tissue factor pathway inhibitor), thrombotic disorders (in combination with an anti-platelet agent or by local delivery through an intracoronary catheter), protein C deficiency, acute arterial thrombotic occlusion, thromboembolism, or stenosis in coronary,
            WPI; 1999-288309/24
                                       Nelsestuen
                                                                    (MINU ) UNIV MINNESOTA
                                                                                                    23-OCT-1997;
                                                                                                                                20-OCT-1998;
                                                                                                                                                              29-APR-1999
                                                                                                                                                                                          W09920767-A1
                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                             therapy.
                                                                                                                                                                                                                                                                                                                                                           GLA domain;
                                                                                                                                                                                                                                                                                                                                                                                      Modified GLA domain of vitamin K-dependent protein
                                                                                                                                                                                                                                                                                                                                                                                                                       17-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY18298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY18298 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cerebral or peripheral arteries or in vascular grafts. Human patients with genetically predisposed prothrombotic disorders may be treated by gene therapy (all claimed):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of a claimed human protein C derivative in which Ser at position 11 of the mature wild-type protein C sequence (see AAB82673) is substituted with Gly, Gln at position 32 with Glu, Asn at position 33 with Asp, Leu at position 194 with Ser, and Thr at position 254 with Ser. It is an example of protein C derivatives of the invention that have at least 2 amino acid substitutions, but which have increased anticoagulant activity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANSFLEELRHGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            419
                                                                                                                                                                                                                                                                                                                                                           mutein;
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                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                  97US-0955636
                                                                                                                                98WO-US22152
                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                       /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapy
                                                                                                                                                                                                                                                                                                                                                          vitamin K-dependent protein; clotting disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63pp;
                                                                                                                                                                                                                        "Xaa= gamma-carboxyglutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (all claimed):
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Pred No. le-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
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                                                                                                                                                                                                                                      acid,
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                                                                                                                                                                                                                                    glutamic
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                                                                                           Query Match
                                                                                                                                                   This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.
                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                       Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders
                                                                            Local
1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                              43;
                                                            Similarity 97.
                                                                                                                                                                                                                                                                                           Page 78;
                                                                                                                      44 AA;
                                                                         87.8%;
97.7%;
                                                                                                                                                                                                                                                                                          English
                                                      Score 173; ив
Pred. No. 1.3e
0; Mismatches
                                                              0
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1.
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44

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RESULT 12
AAY18299
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                                                                                                                                                                                            GLA domain;
                                                                                                                20-OCT-1998;
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                                                                                                                                     WO9920767-A1
                                                                                                                                                              Key
                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                      Modified GLA
                                                                                                                                                                                                                17-AUG-1999
                                                                                                                                                                                                                          AAY18299
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                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                      therapy.
                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                            mutein;
                                                                                                                                                                                                      domain
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                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                    /note=
                                                                                                                                                                                                                                    peptide;
                                                                                                                                                                                                     of vitamin K-dependent protein
                                                                                                                                                                                                                entry)
                                                                                                                                                                                            vitamin K-dependent protein; clotting disorder;
                                                                                                                                              "Xaa= gamma-carboxyglutamic acid"
                                                                                                                                                                                                                                     44
                                                                                                                                                   acid,
                                                                                                                                                   or glutamic
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to the native polypeptide. The polypeptide is used to disorder by decreasing or increasing clot formation. w GLA domain results in a protein which has enhanced mem affinity as compared to the native protein.

domain. The invention relates to a vitamin K-dependent polypept comprising a modified GLA domain containing an amino acid substwhich enhances membrane binding of the modified polypeptide as

ependent polypeptide amino acid substitution

Modification eptide as compared treat a clotting Modification of the This sequence represents a modified GLA (gamma-carboxyglutamic acid)

Claim

8,

Page

78;

86pp;

English.

Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders

WPI; 1999-288309/24

Nelsestuen

(MINU ) UNIV MINNESOTA

23-OCT-1997;

97US-0955636

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RESULT 13
AAY18307
ID AAY18
AC AAY18307
AC AAY18
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                                                                                                                                                                                                                                                                  which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.
                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a modified GLA (gamma-carboxyglutamic actionmain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitute.
                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 79; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09920767-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLA domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified GLA domain
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                                                                                 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                             ANSFLXXLRDSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
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42; Conser
                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of vitamin K-dependent protein.
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Pred. No. 4.
                                                                                                                                             Score 168; DB 20;
Pred. No. 9.1e-21;
0; Mismatches 2
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RESULT 14

Homo sapiens

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RESULT 15
AAY18309
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XX
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AC AAY1
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AXX
AXX
DT 17-A
XX
KW GLA
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XX
Homc
OS Synth
XX
FT Miss
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AAY18297
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Best Local S
Matches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 78; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-AUG-1999
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therapy.
                              GLA domain; mutein;
                                                                                                                                                                     17-AUG-1999
                                                                                                                                                                                                                                                                                                AAY18309 standard; peptide; 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a modified GLA (gamma-carboxyglutamic acid)
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                                                                                                   Modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
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                                                                                                GLA domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 AA;
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                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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acid"
                              vitamin K-dependent protein; clotting
                                                                                                of vitamin K-dependent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vitamin K-dependent protein; clotting disorder;
                                                                                                                                                                 entry)
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Pred. No. 9.1e-21;
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                                  disorder;
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Search completed: May 16, 2003, 10:14:32 Job time: 36 secs
                                                       В
                                                                               Qy
                                                                                                                                                                 Query Match 81.2%;
Best Local Similarity 93.2%;
Matches 41; Conservative
                                                                                                                                                                                     This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key Location/Qualifiers
Misc-difference 1.44
/note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                              Disclosure; Page 79-80; 86pp; English.
                                                                                                                                                                                                                                                                                                                                      Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders
                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-288309/24.
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                                                   44 AA;
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                                                                                                        Score 160; DB 20
Pred. No. 2e-19;
0; Mismatches
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                                                                                                                                   Length 44;
                                                                                                          Indels
                                                                                                          0
                                                                                                       Gaps
                                                                                                        0;
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OM protein - protein search, using sw model

Run on: May 16, 2003, 10:12:44; Search time 18 Seconds (without alignments)
234.995 Million cell updates/sec

Title SEQ1-4EDITS

Perfect score: Sequence: ANSFLXXLRqgSLXRXCIXX.....XXAKXIFedVDDTLAFWSKH

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters:

283224

Minimum DB seq length: Maximum DB seq length: length: 2000000000 0

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database PIR\_73:\* pir1:\*
pir2:\*
pir3:\*

p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10		8	7	6	5	4	ω	N	_	Result	
65		69.5	~	72	73	78	78	80	80	80	80	81	84	85	85	88	86	86.5	86.5	99	101	110	114	115	122	139	140	160	Score	
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A48089	KXHUZ .	KXB0Z	KXMSS	TBBO	KFBO	KXRTS	S53433	KXBOS	KFHU	JQ0419	A30351	S38819	TBHU	KXHUS	S53434	KFB07	EXCH	A35827	S10511	KFHU7	146932	EXHU	EXBO	EXRT	KXBO	S18994	JX0210	KXHU	ID	
growth arrest-spec	protein	2	plasma proteľn S p	thrombin (EC 3.4.2	coagulation factor	ໝ	S	æ	coagulation factor	coagulation factor	coagulation factor	<ul> <li>plasma protein S -</li> </ul>	thrombin (EC 3.4.2	plasma protein S p	plasma protein S p	coagulation factor	coagulation factor		thrombin (EC 3.4.2			coagulation factor	ion	tior	o o	protein C (activat	protein C (activat	protėin C (activat	Description	

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674 2 155476 growth potent 678 2 B48089 growth arrest 594 2 D84859 probable MAP 603 2 C95675 probable MAP 576 2 G96763 probable MAP 606 2 T40556 probable MAP 606 2 T40556 probable MAP 607 2 T303367 protein-tyrol 323 2 T25948 protein-tyrol 323 2 T25948 protein-tyrol 323 2 T35936 protein-tyro	protein-tyrosine k	•	A48999	N	1298	24.4	48	2
674 2 155476 growth potent 674 2 1848089 growth arrest 578 2 B48089 probable MAP 603 2 C96575 probable MAP 606 2 T40556 probable MAP 606 2 T023575 probable MAP 606 2 T023575 protein-tyro: 1363 2 158375 protein-tyro: 1363 2 158	VSG expression sit		D32433	2	1235	24.4	48	Ξ
674 2 155476 678 2 B48089 594 2 D84859 603 2 C96575 678 2 G96763 606 2 T40556 11684 2 T03367 116	mitogen-activated		T39306	N	422	24.4	48	5
674 2 155476 growth potent 678 2 B48089 growth arrest 594 2 D84859 probable MAP 603 2 C96575 probable MAP 576 2 G96763 probable MAP 606 2 T40556 hypothetical 1684 2 T02367 hypothetical 1363 2 158375 protein-tyrost 323 2 T25948 hypothetical	ammonium transport		E82918	N	510	24.6	48.5	9
674 2 155476 growth potent 678 2 B48089 growth arrest 578 2 D84859 probable MAP 603 2 C96575 probable MAP 576 2 G96763 probable MAP 606 2 T40556 probable MAP 606 2 T02367 hypothetical 1363 2 158375 protein tyrot	hypothetical prote		T25948	N	323	24.6	48.5	æ
674 2 155476  678 2 B48089  594 2 D84859  603 2 C96575  576 2 G96763  606 2 T40556  1684 2 T02367  607 9 probable MAP  608 1 MAP  609 probable MAP	protein-tyrosine k	•	158375	N	1363	24.9	49	37
674 2 155476 · 678 2 B48089 594 2 D84859 603 2 C96575 576 2 G96753 606 2 T40556			T02367	N	1684	25.4	50	8
674 2 155476 678 2 B48089 603 2 C96575 576 2 G96763			T40556	N	606	26.9	53	5
674 2 155476 · 678 2 B48089 594 2 D84859 603 2 C96575	MAP	`	G96763	N	576	27.2	53.5	4
674 2 155476 · 678 2 B48089 594 2 D84859	•		C96575	N	603	27.7	54.5	ω
674 2 155476 678 2 B48089	-		D84859	N	594	28.7	56.5	ລ
674 2 I55476	arres		B48089	2	678	32.0 .	63	3
	growth potentiatin		<b>I</b> 55476	N	674	32.5	64	ŏ

## ALIGNMENTS

HO i .	
otein C (activated) (EC 3.4.21.69) precursor - human	
Alternate names: autoprothrombin IIA; plasma protein C	
Species: Homo sapiens (man)	
Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999	
Accession: A22331; A25426; A21781; A23789; A00927	
Foster, D.C.; Yoshitake, S.; Davie, E.W.	
oc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985	
Title: The nucleotide sequence of the gene for human protein C.	
Reference number: A22331; MUID:85270390; PMID:2991887	
Accession: A22331	
Molecule type: DNA	
Residues: 1-461 <fos1></fos1>	

Pro

A;Cross-references: GB:M11228; NID:g190333; PIDN:AAA60166.1; PID:g190334 R;Plutzky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R. Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986 A;Title: Evolution and organization of the human protein C gene. A;Reference number: A25426; MUID:86120978; PMID:3511471

A; Molecule type: DNA A; Accession: A25426

R; Foster, D.; Davie, E.W. A;Residues: 1-445,'L',446-461 <PLU> A;Cross-references: GB:M12712; NID:g190330; PIDN:AAA60165.1; PID:g190332

Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984
A; Title: Characterization of a cDNA coding for human protein C.
A; Reference number: A21781; MUID:84272714; PMID:6589623

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A; Accession: A21781

A;Molecule type: mRNA
A;Residues: 'Q',107-461 <FOS2>
A;Residues: 'Q',107-461 <FOS5; NID:g190322; PIDN:AAA60164.1; PID:g190323
A;Cross-references: GB:K02055; NID:g190322; PIDN:AAA60164.1; PID:g190323
R;Beckmann, R.J.; Schmidt, R.J.; Santerre, R.F.; Plutzky, J.; Crabtree, G.R.; Long, (Nucleic Acids Res. 13, 523-5247, 1985
A;Title: The structure and evolution of a 461 amino acid human protein C precursor all Reference number: A23789; MUID:85269639; PMID:2991859

A; Accession: A23789

A; Molecule type: mRNA A; Residues: 1-461 <BEC>

A: Cross-references: GB: X02750; NID: 935689; PIDN: CAA26528.1; PID: 9763120

R: Milettch, J.P.; Broze Jr., G.J.

J. Biol. Chem. 265, 11397-11104, 1990

A: Title: Beta protein C is not glycosylated at asparagine 329. The rate of translatic A: Reference number: A44605; MUID: 90293094; PMID: 1594179

A: Contents: annotation; carbohydrate binding sites; activation peptide A: Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is R: Harris, R.J.; Ling, V.T.; Spellman, M.W.

J. Biol. Chem. 267, 5102-5107, 1992

A: Title: O-linked fucose is present in the first epidermal growth factor domain of final Reference number: A44606; MUID: 92184750; PMID: 1544894

A; Contents:

ivation Protein C annotation; beta-hydroxyaspartic acid protein C is the zymogen of the vitamin K-dependent serine proteinase that factor Va is strongly enhanced by complexing with protein S. Protein C al:

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F;212-445/Domain: trypsin homology <TRY>
F;47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #st
F;112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F;121-130,139-150,146-159,161-174,182-319,238-254,373-387,398-426/Disulfide bonds:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #tewt_change 16-Jun 2000
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                                                                                                                                                                                                                                                                            F;199-461/Domain: heavy chain #status predicted <PCH>F;199-211/Domain: activation peptide #status predicte
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F;110/Binding site: carbohydrate (Thr) (covalent) #status absent
F;113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Comment: Protein C is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: JX0210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Isolation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:D10445; NID:g220385; PIDN:BAA01235:1; PID:g220386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-461 <TAD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 2q13-2q21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                    42-196,199-461/Product: protein C #status predicted;42-196/Domain: light chain #status predicted <PCL>
91-130/Domain: Egg homology <EG1>
139-174/Domain: PCE box 139-174/Domai
                                                                                                                                                                                                                                                                                                                                                                139-174/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superfamily: coagulation factor X; EGF homology; Gla dor Keywords: beta-hydroxyaspartic acid; blood coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;139,290,355/Binding site: carbohydrate (Asn) (covalent) #statu
;211-212/Cleavage site: Arg-Leu (thrombin) #status experimental
;253,299,402/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43-197/Product: protein C light chain #status predicted <LCH>92-131/Domain: ECF homology <EG1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1; Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin; Superfamily: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calciu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-33/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :33-42/Domain: propeptide #status predicted <PRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48,49,56,58,61,62,67,68,71/Modified site: gamma-carboxyglutamic acid (Glu) #status e
59-64,92-105,101-120,122-131,140-151,147-160,162-175,183-319,238-254,373-387,398-426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200-461/Product: protein C heavy chain #status predicted'<HCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-85/Domain: Gla domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200-211/Domain: activation peptide #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-86/Domain: Gla domain homology <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-32/Domain: signal
                                 4,290,355/Binding site: carbohydrate
                                                                                                                                                                                                                                      2-461/Product: vitamin K-dependent serine proteinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2-445/Domain: trypsin homology <TRY>,49,56,58,61,62,67,68,71/Modified site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.; Sato,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75/Domain: EGF homology <EG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKH 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (activated) (EC 3.4.21.69) precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cleaves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             names: vitamin K-dependent serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , M.; Tsujimura, A.; Iwase, 491-495, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                           EGF homology <EG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           മറ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                characterization of 0210; MUID:92316897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.2%;
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Pred. No. 8.8e-18;
Ser #status
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                                     (Asn) (covalent).
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PMID:1618739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.; Hashimoto-Gotoh,
                                                                                                                                                                                                                                                                                predicted
predicted
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of the
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heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        binding; carboxygluta
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                                                                                                                                              (Glu) #status
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K;Okatuji, T.; Maekawa, K.; Nawa, K.; Maru
Biochim. Biophys. Acta 1131, 329-332, 1992
A;Title: The cDNA cloning and mRNA express:
A;Reference number: S24312; MUID:92329550;
A;Accession: S24312
A;Status: preliminary
                                                               A; Title: Cloning and sequence of 1 A; Reference number: A26250; MUID: 8
                                                                                                                                                      C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Nov-1980 #sequence_revision 17-Mar-1987
C;Accession: A26250; A18385; A18386; A00928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;33-42/Domain: propeptide #status predicted <PRO>
F;43-461/Product: protein C #status predicted <PRC:
F;41-10/Domain: EGF homology <EG1>
F;139-174/Domain: EGF homology <EG2>
A; Molecule type: mRNA
A; Residues: 1-456 <LON>
                                               A; Accession: A26250
                                                                                                              Proc.
                                                                                                                                 R; Long,
                                                                                                                                                                                                                               N;Alternate
                                                                                                                                                                                                                                                    protein C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;213-445/Domain: trypsin homology <TRY>
F;47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Keywords: beta-hydroxyaspartic acid; glycoprotein;
F;1-32/Domain: signal sequence #status predicted <SIO
F;27-85/Domain: Gla domain homology <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Date: 10-Sep-1999 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein C (activated) (EC 3.4.21.69) precursor - C;Species: Rattus norvenione (no.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X64336; NID:g56962; PIDN:CAA45617.1; R;Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Okafuji, T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: S18994; S24312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X64336; NID:g56962; PIDN:CAA45617.1; PID:g56963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted ;112/130,139-150,146-159,161-174,182-320,239-255,373-387,398-426/Disulfide bonds:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215,291,355/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                              Natl.
                                                                                                                                                                                                                                                                                                                                                                  42 ANSFLEEVRAGSLERECMEEICDFEEAQEIFQNVEDTLAFWIKY
                                                                                                                                 G.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42
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                                                                                                                                                                                                                                                  (activated) (EC 3.4.21.69)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANSFLEEMRPGSLERECMEEICDFEEAQEIFQNVEDTLAFWIKY 85
                                                                                                              Acad.
                                                                                                                                                                                                                     names: autoprothrombin IIA; plasma b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-461 <OKA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                         Balagaje, R.M.; MacGillivray, R.T.A. cad. Sci. U.S.A. 81, 5653-5656, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The cDNA cloninig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maekawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K.; Nawa, K.; Marumoto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.6%;
59.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mRNA expression of rat protein 2; MUID:92329550; PMID:1627650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.18; 59.18;
                                                                      MUID:85014826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Asp,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 139; DB 1;
Pred. No. 2.1e-14;
7; Mismatches 11
                                                                                         5653-5656, 1984
iver cDNA coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 140;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                February 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <PRC>
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                                                                                                                                                                           #text_change 16-Jul-1999
                                                                                           for bovine
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                                                                                         protein
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homo1

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J. Blol. Chem. 257, 1
A;Title: Amino acid s
A;Reference number: A
A;Accession: A18385
A;Molecule type: prot
A;Residues: 40-194 <F
                                coagulation factor XA (recorded in the coagulation factor XA (recorded in the coagulation factor XA)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Jan-1995 #sequence_revision 07-Feb
C;Accession: $49075; JC4670; PS0191; PS0190;
C;Accession: C: Ross, P.; Hutson, S.; Wallin, Thromb. Res. 80, 63-73, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F:34-83/Domain: Edy domain homology <CLAS
F:30-39/Domain: propeptide #status predicted <PRO>
F:40-194/Product: protein C light chain #status experimental <LCH>
F:40-194/Product: protein C light chain #status experimental <LCH>
F:98-128/Domain: EGF homology <EGI>
F:98-128/Domain: EGF homology <EGI>
F:137-172/Domain: EGF homology <FGI>
F:197-210/Domain: activation peptide #status experimental <HCH>
F:197-10/Domain: activation peptide #status experimental <APT>
F:211-440/Domain: trypsin homology <TRY>
F:211-440/Domain: trypsin homology <TRY>
F:45,46.53,55.58,59,62,64,65.68,74/Modified site: gamma-carboxyglutamic acid (Glu) #status F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:119-128,137-148,144-157,159-172,180-318,237-253,368-382,393-421/Disulfide bonds: #status F:252,288,397/Active site: carbohydrate (Asn) (covalent) #status predicted
F:252,288,397/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cognition of the thrombin-thrombomodulin complex. C:Comment: The gamma-carboxyglutamic acid residue: C:Superfamily: coagulation factor X: EGF homology C:Keywords: anticoagulant: beta-hydroxysspartic as F:1-29/Domain: signal sequence (fragment) #status F:1-29/Domain: Gla domain homology <GLA>
F:30-39/Domain: propeptide #status predicted <PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Comment: Protein C is synthesized in the liver as a single chain precursor, which is bin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this react C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Structural changes required for activation of protein C are induced by C A;Reference number: A37542; MUID:83213514; PMID:6406503 A;Contents: annotation; activation; calcium binding C;Comment: Protein C is the zymogen of the vitamin.K-dependent serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Esmon, N.L.; DeBault, L.E.; Esmon, C.T.
J. Biol. Chem. 258, 5548-553, 1983
A;Title: Proteolytic formation and properties of gamma-carboxyglutamic A;Reference number: A37541; MUID:83213513; PMID:6304092
A:Contents: annotation; activation; calcium binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R:Stenflo, J.; Fernlund, P.
J. Blol. Chem. 257, 12180-12190, 1982

A:Title: Amino acid sequence of the heavy chain of bovine A;Reference number: A18386; MUID:83007326; PMID:6896877

A:Accession: A18386
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A;Title: beta-Hydroxyasparttc acid in vitamin K-dependent protein A;Reference number: A19316; MID:83169; PMID:6572939
Thromb. Res. 80, 63:
A;Title: Evidence fo
A;Reference number:
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R; Stenflo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitaming Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology; Superfamily: coagulation; beta-hydroxyaspartic acid; blood coagulation; calcium binding Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-29/Domain: signal sequence (fragment) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: protein Residues: 197-454, 'PV' <STE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contents: annotation; revision to residue Stenflo, J.; Fernlund, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Residues: 40-194 <FER>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWS 42
                                                                                                                                                                                                                                                                                                                                                                                                                    ANSFLEELRPGNVERECSEEVCEFEEAREIFQNTEDTMAFWS
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sequence of the light chain of bovine protein
A18385; MUID:83007325; PMID:6896876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carbohydrate
   competition between vitamin K-dependent clotting factors 8498; MUID:96093366; PMID:8578539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.9%;
                                                                                                                                                                                                                                            3.4.21.6) precursor -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 122; DB:
Pred. No. 1.2e-1
9; Mismatches
                                                                                                                                                                        07-Feb-1997 #text_change
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coagulation factor Xa (EC 3.4.21.6) precursor NyAlternate names: Stuart factor C;Species: Bos primigenius taurus (cattle) C;Date: 24-Apr-1984 #sequence_revision 17-Mar-
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41

ANSFFEEIKKGNLERECVEEICSFEEAREVFEDNEKTTEFWNKY

84

genius taurus (cattle) #sequence\_revision 17-Mar-1987

#text\_change

16-Jul-1999

bovine

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A; Molecule type: protein
A; Residues: 183-186, 'X', 188-207 <ENJ2>
R; Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Hara
Eur. J. Haematol. 52, 162-168, 1994
A; Title: Analysis of the partial nucleotide sequences and
A; Reference number: 146196; MUID:94222160; PMID:8168596
A; Accession: 162745
                                                                                                                                                          F:187/Binding site: carbohydrate (Asn) (covalent) #status experimental F;208/Binding site: carbohydrate (Thr) (covalent) #status predicted F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted F;231-332/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation F;274,320,417/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Pathway: blood coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 295-383,'G',385-455 <MUR>
A;Cross-references: GB:D21215; NID:g415309; PIDN:BAA04756.1; PID:g455396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: pro
A; Residues: 41-58,';
A; Accession: PS0190
                                                                                                                                                                                                                                                                                         F;232-460/Domain: trypsin homology <TRY>
F;46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu)
F;57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-340,238-243,259-275,388-4
F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                           F;129-164/Domain: EGF homology <EG2>
F;183-482/Product: coagulation factor X heavy chain #status F;183-231/Domain: activation peptide #status predicted <APT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; F;1-23/Domain: signal sequence *status predicted <SIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X79807: NII:g506600; PII
A;NOTE: submitted to the EMBL Data Library, June
A;NOTE: nelther the complete nucleic acid sequenc
R;Stanton, C; Ross, R.P.; Hutson, S.; Wallin, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;41-179/Product: coagulation factor X F;90-121/Domain: EGF homology <EG1>
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                                                                                                                                                                                                                                                                                                                                                                                                    F;232-482/Product: coagulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X79807; NID:g506600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-482 < STA2>
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1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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269-273, 1
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A; Accession: Allow, V, 104-180 CENES
A; Molecule type: protein
B; Mol
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R;FUjlkawa, K.; Titani, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 72; 3359-3363, 1975
A;Title: Activation of bovine factor X (Stuart factor):
A;Reference number: A13504; MUID:76053121; PMID:1059122
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A; Title: Bovine factor X-la (activated Stuart factor). Evidence of A; Reference number: A12453; MUID:73053314; PMID:4264286
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A;Molecule type: protein
A;Residues: 183-292,294-295, 'GDE',299-334,336-348, 'AE',351-354,356-441, 'GKEG',446-492 < A;Residues: 183-292,294-295, 'GDE',299-334,336-348, 'AE',351-354,356-441, 'GKEG',446-492 < A;Residues: 183-292,294-295, 'GDE',299-334,36-348, 'AE',351-354,356-441, 'GKEG',446-492 < A;Residues: 183-292,294-394, 'GEE,354-354, 'GEE,354, 'GEE,354, 'GEE,354, 'GEE,354, 'GE
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A; Reference number: A38025; MUID:86140210;
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A; Title: Calcium-binding
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J. Biol. Chem. 259, 5705-5710, 1984
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A; Residues: 183-
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Eur. J. Biochem. 218, 153-163, 1993
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                                                                                                                                                              Factor Xa converts prothrombin to thrombin during blood clotting. The two chains are formed from a single-chain precursor by the ex The activation peptide is cleaved by factor IXa (in the intrinsic
                                                                            Calcium binds
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A.; Neurath,
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F:218/Binding site: carbohydrate (Asn) (covalent) #status experimental F:233-234/Cleavage site: Arg Tle (coagulation factor IXa, coagulation factor VIIa) F:240-245,260-276,389-403,414-442/Disulfide bonds: #status experimental F:275,321,418/Active site: His, Asp, Ser #status predicted F;234-461/Domain: trypsin homology <TRY>
F;464,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid ((F;57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-341/Disulfide bonds: #si
F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F;200/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
F;200/Binding site: carbohydrate (Thr) (covalent) #status experimental F;41-180/Product: coagulation factor x light chain \*status experimental <LCH> F;90-121/Domain: EGF homology <EGI> F;129-164/Domain: EGF homology <EGI> F;129-164/Domain: EGF homology <EGI> F;13-492/Product: coagulation factor x heavy chain \*status experimental <HCH> F;183-492/Product: coagulation peptide \*status experimental <APT> F;183-233/Domain: activation peptide \*status experimental <APT> F;234-492/Product: coagulation factor x heavy chain \*status experimental <AHC> F;234-492/Product: coagulation factor x heavy chain \*status experimental <AHC> F;234-492/Product: coagulation factor x heavy chain \*status experimental <AHC> F;234-492/Product: coagulation factor x heavy chain \*status experimental <AHC> F;234-492/Product: coagulation factor x heavy chain \*status experimental <AHC> F;234-492/Product: coagulation factor x heavy chain \*status experimental <AHC> F;234-492/Product: coagulation factor x heavy chain \*status experimental <AHC> F;234-492/Product: coagulation factor x heavy chain \*status experimental <AHC> F;234-492/Product: coagulation factor x heavy chain \*status experimental <AHC> F;234-492/Product: coagulation factor x heavy chain \*status experimental <AHC> F;234-492/Product: coagulation factor x heavy chain \*status experimental <AHC> F;234-492/Product: coagulation factor x heavy chain \*status experimental <AHC> F;234-492/Product: coagulation factor x heavy chain \*status experimental <AHC> F;234-492/Product: coagulation factor x heavy chain \*status experimental <AHC> F;234-492/Product: coagulation factor x heavy chain \*status experimental <AHC> F;234-492/Product: coagulation factor x heavy chain \*status experimental <AHC> F;234-492/Product: coagulation factor x heavy chain \*status experimental <AHC> F;234-492/Product: coagulation factor x heavy chain \*status experimental <AHC> F;234-492/Product: coagulation factor x heavy chain \*status experimental <AHC> F;244-492/Product: coagulation factor x heavy chain \*status experimental <AHC> F;244-492/Product: coagulation factor x heavy chain \*status experiment F;16-40/Domain: propeptide #status predicted <PRO>F;25-84/Domain: Gla domain homology <GLA> C; Keywords: beta-hydroxyaspartic F;1-15/Domain: signal sequence #status predicted <SIG> A; Pathway: blood coagulation A; Description: Matches Superfamily: coagulation factor X; Local Similarity catalyzes the proteolytic activation Conservative 57.9%; 45.5%; 8; Mismatches acid; blood coagulation; Score 114; Pred. No. 2 EGF homology; Gla domain homology; tr:d; blood coagulation; calcium binding; DB .5e-5 0f Length 492; Indels prothrombin 0; to thrombin Gaps trypsin homol ng; carboxyglu

(Glu)

ANSFLEEVKQGNLERECLEEACSLEEAREVFEDAEQTDEFWSKY 84 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH . 44 0,

C;Species: Homo sapiens (man)
C;Date: 15-Nov-1984 #sequence\_revision 02-May-1994 #text\_change 08-Dec-2000
C;Accession: A24478; JQ0917; A42485; A25853; A22208; A21284; A20362; S39415;
R;Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.
Biochemistry 25, 5098-5102, 1986 A; Reference number: A24478; A; Title: Gene for human N;Alternate coagulation factor Xa (EC 3.4.21.6) names: Stuart factor Factor X: a blood coagulation factor 478; MUID:87026600; PMID:3768336 precursor [validated] human whose gene organization I54051;

A;Cross-references: GB:L29433; GB:M14327; NID:9459809; PIDN:AAA52764.1; R;Messier, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R. A; Molecule type: DNA A; Residues: 1-488 <LEY>

PID:g182831

A; Reference number: JQ0917; A; Accession: JQ0917 Gene 99, 291-294, 1991 A; Title: Cloning and e expression in COS-1 cells of a full-length MUID:91216473; PMID:1902434 cDNA encoding human

PID:g182390

A; Molecule type: mRNA A; Residues: 1-488 < MESS | A; Cross-references: GB: M57285; NID:g182389; PIDN:AAA52421.1; A; Cross-references: GB: M57285; NID:g182389; PIDN:AAA52421.1; R; Miao, C.H.; Leycus, S.P.; Chung, D.W.; Davie, E.W. J. Biol. Chem. 267, 7395-7401, 1992 A; Title: Liver-specific expression of the gene coding for hum A; Reference number: A42485; MUID:92218390; PMID:1313796 A; Accession: A42485 human factor X, a

A; Molecule type: DNA A; Residues: 1-15 <MIA>

A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIN:93780, R;Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P Gene 41, 311-314, 1986
A;Title: Isolation and characterization of human blood-coag A;Reference number: A25853; MUID:86221713; PMID:3011603 NCBIP: 93787)

A; Accession: A25853

human blood-coagulation

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A;Cross-references: GDB:119890; OMIM:227600
A;Map position: 13934-13934
A;Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
A;Note: deficiency of this factor causes Stuart disease C;Function:
A;Description: catalyzes the proteolytic activation of prot A;Pathway: blood coagulation
C;Superfamily: coagulation
C;Superfamily: coagulation factor X; EGF homology; Gla doma C;Keywords: beta-hydroxyaspartic acid; blood coagulation; C;Keywords: beta-hydroxyaspartic acid; blood coagulation; F;1-23/Domain: signal sequence #status predicted <SIC>F;24-40/Domain: propeptide #status predicted <PRO>F;25-84/Domain: Gla domain homology <GLA>F;41-179/Product: coagulation factor X light chain #status F;40-121/Domain: EGF homology <EG1>F;90-121/Domain: EGF hom
      F;24-40/Domain: propeptide #status predicted <SIG>
F;25-84/Domain: propeptide #status predicted <PRO>
F;25-84/Domain: Gla domain homology <GLA>
F;41-179/Product: coagulation factor X light chain #status experimental <LCH>
F;90-121/Domain: EGF homology <EGI>
F;129-164/Domain: EGF homology <EGI>
F;183-348/Product: coagulation factor X heavy chain #status experimental <HCH>
F;183-34/Domain: activation peptide #status experimental <APT>
F;235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>
F;235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>
F;235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>
F;235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>
F;235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>
F;35-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>
F;365-489/Product: coagulation factor Xa heavy chain #status experimental <ACT>
F;365-489/Product: coagulation factor Xa heavy chain #status experimental <ACT>
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F;365-489/Product: coagulation factor Xa heavy chain #status experimental <ACT>
F;365-489/Product: coagulation factor Xa heavy chain #status experimental <ACT>
F;366,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu)
F;5762/Disulfide bonds: #status predicted
F;90-101,95-110,112-121.129-140 136-140
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A; Residues: 13-441'S', 443-488 <FUNS
A; Residues: 13-441'S', 443-488 <FUNS
A; Cross references: GB:K03199; NID:g182840; PIDN:ANA5245
A; Cross references: GB:K03199; NID:g182840; FIDN:ANA5245
B; Leytus, S.P.; Chung, D.W.; Kisiel, W.; Kurachi, K.; Dc
Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984
A; Title: Characterization of a cDNA coding for human fac
A; Reference number: A21284; MUID:84222026; PMID:6587384
A; Accession: A21284.
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A;Title: Characterization of an almost full-length cDNA coding A;Reference number: A22208; MUID:85216545; PMID:2582420
A;Accession: A22208
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R;Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Bli J. Mol. Biol. 232, 947-966, 1993
A;Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.
A;Reference number: A49458; MUID:93360277; PMID:8355279
A;Contents: annotation; X-ray crystallography, 2.2 angstroms
C;Comment: The two chains held together by one disulfide bond are formed from a single-c;Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) of the comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) of the comment: The works and the cleaved by factor IXa (in the intrinsic pathway) of the comment is the control of th
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A;Title: Cloning and characterization of the 5' end (exon 1)
A;Reference number: I54051; MUID:90128299; PMID:2612918
A;Accession: I54051
A;Accession: I54051
A;Status: 'translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-23 <RES>
A;Cross-references: GB:M33297; NID:g183860; PIDN:AAA52636.1;
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A; Residues: 183-234 < INO>
A; Residues: 183-234 ton sites
A; Note: glycosylation sites
A; Note: identification and characterization of beta-hydroxyaspartic acid
R; Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhushanam, K.; Lyman, C
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A;Title: Complete amino acid sequence of the light chain A:Reference number: A20362; MUID:83257207; PMID:6871167
A;Accession: A20362
A;Molecule type: protein
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A;Residues: 13-284,'E',289-488 <LE2>
A;Cross-references: GB:K01886
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Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutar
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Blochem. 218, 153-163, 1993
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: #status predicted
,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/
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E.W.
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В

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ANSFLEELRPGSLERECKEELCSFEEAREVFQSTERTKQFW

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coagulation factor VII - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997
C:Accession: 146932
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                                                                                                                                                              C;Superfamily: coagulation factor X; EGF F:24-83/Domain: Gla domain homology <GLA> F:89-120/Domain: EGF homology <EG2> F:130-166/Domain: EGF homology <EG2>
                                                                                                                                                                                                                                                                                                                                               A;Title: Complete nucleotide sequence of the cDNA encoding A;Reference number: I46932; MUID:93190306; PMID:8383365 A;Accession: I46932
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Q
                                                                                                                                      F;130-166/Domain: EGF homology <EG2>
F;192-425/Domain: trypsin homology <TRY>
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                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-443 <BR
                                                                                                                                                                                                                                                                                                                                                                                                                  R;Brothers, A.B.; Clarke, B.J.; Sheffield; W.P.; Blajchman, Thromb. Res. 69, 231-238, 1993
                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                  Matches
                                                                                          Query Match
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                                                                       Best
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    1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFW 41
                                                                                                                                                                                                                                                                              1-443 <BRO>
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19; Conservative
                                                                       Similarity
                                                  Conservative
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te: carbohydrate (Thr) (covalent) #status experimental
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                                                                   51.3%;
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Pred. No. 1.1e-09
                                                                     Score 101;
Pred. No. 2.
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                                                                       DB 2;
.8e-08;
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A;Cross-references: GB:J02933; NID:g180333; PIDN:AAA51983.1; R;Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G. Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986 A;Title: Characterization of a CDNA coding for human factor V A;Reference number: A23819; MUID:86205965; PMID:3486420 coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human
C; Species: Homo sapiens (man)
C; Date: 19-May-1989 #sequence\_revision 19-May-1994 #text\_change 08-Dec-2000 A; Title: Amino acid sequence A: Reference number: A90539; M A;Cross-references: GB:M13232; NID:g182799; PIDN:AAA88040.1; R;Thim, L.; Bjoern, S.; Christensen, M.; Nicolaisen, E.M.; Li Biochemistry 27, 7785-7793, 1988 C;Accession: A28322; A23819; A31186; B31186; R;O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, A; Molecule type: mRNA A; Residues: 1-466 < HAG> A; Molecule type: DNA A; Residues: 1-466 < OHA> A; Accession: A23819 A; Accession: A28322 A; Reference number: A28322; A; Title: Nucleotide sequence of the protein e of the gene coding for human MUID:87260948; PMID:3037537 and posttranslational modifications MUID:89088153; PMID:3264725 coding for human factor VII. PMID: 3486420 Gray, C.L.; Insley, M.Y.; 1987 S63524 factor Lund-Hansen, PID: g182801 PID: 9180334 VII, Ö, Woodbury, human a vitamin Hagen, factor ж.G.; F.S.; N K-dep Hart

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RESULT 10
S10511
thrombin (EC
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                                                                                R; Henrikson, K.P.; Jazin, E.E.; G
Endocrinology 126, 167-175, 1990
                                                                                                                          A; Cross-references:
                                                                                                                                             A; Residues:
                                                                                                                                                                                       Nucleic Acids Res. 18, 4251, 1990
A;Title: CDNA sequence of rat prothrombin.
A;Reference number: S10511; MUID:90332426;
A;Accession: S10511
                                                                                                                                                                                                                                                                                                           thrombin (EC 3.4.21.5) precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 03-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GDB:119897; OMIM:227500
A;Map position: 13q34-13q34
A;Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1
C;Function:
                                                                                                                                                               A; Molecule type:
                                                                                                                                                                                                                                                                            R;Dihanich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oagulation factor IX in the presence of calcium and tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description:
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A; Residues: 61-65; 99-103; 105-109; 213-217; 308-312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Human plasma and recombinant factor VII. Chara A; Reference number: A40529; MUID:91250411; PMID:1904059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Pathway: blood coagulation extrinsic pathway
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A;Accession: B3118
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                                                                                                                                                                                                                                                                                             ; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superfamily: coagulation factor x; EGF homology; Gla domain homology; tr; Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFW 41
                                                                                                                                           1-617 <DIH>
                                                                                                                                                                                                                                                                          M.; Monard,
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                                                                                                                                                                     mRNA
protein
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                                                                                                  EMBL:X52835; NID:g56969; PIDN:CAA37017.1; Jazin, E.E.; Greenwood, J.A.; Dickerman, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.3%;
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Pred. No.
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                                         in the estrogen-treated; PMID:2293980
                                                                                                                                                                                                           PMID: 2377469
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R;Degen, S.J.F
-- DNA Cell Biol.
F;50,51,58,60,63,64,69,70,7
F;61-66,91-104,109-187,130-
F;403,459,565/Active site:
                                                                                                                                                                                                                                   F;44-618/Product:
F;109-187/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology C;Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprote F;1-24/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 384-618, 'E' <BAN>
A; Cross-references: GB: M81394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A;Title: Partial characterization of vertebrate partial characterization of vertebraterization of vertebraterization of vertebraterization of vertebraterization of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A35827; A; Accession: A35827
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C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 03-May-2002
C;Accession: A35827; A42696; S12081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;44-617/Product: prothrombin #status experimental <PMAT>
F;109-187/Domain: kringle homology <KR1>
F;2109-187/Domain: kringle homology <KR2>
F;215-292/Domain: kringle homology <KR2>
F;360-609/Domain: trypsin homology <TRY>
F;50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F;61-66,91-104,109-187,130-170,158-182,215-292,236-276,264-287,332-478,387-403,532-54
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                                                                                                                                                                                                                                                                                                                                      F;25-43/Domain: propeptide #status predicted <PRO>F;28-88/Domain: Gla domain homology <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: A42696; MUID:92212913; A;Accession: A42696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: the data were obtained from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-618 <DEG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombin (EC 3.4.21.5) precursor - mouse
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A; Residues: 383-617, 'E' <BAN>
A; Cross-references: GB: M81397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 44-58 <HEN>
A; Note: the authors purified the proenzyme R; Banfield, D.K.; MacGillivray, R.T.A. Proc. Natl. Acad. Sci. U.S.A. 89, 279-2783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;25-43/Domain: propeptide #status predicted <PRO>F;28-88/Domain: Gla domain homology <GLA>
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                                            ;109-187/Domain: kringle homology <KR1>;215-293/Domain: kringle homology <KR2>;315-293/Domain: kringle homology <TRY>;361-610/Domain: trypsin homology <TRY>
;50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #stat;50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #stat;50-65,91-104,109-187,130-170,158-182,215-293,236-276,264-288,333-479,388-404,533-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Schaefer, L.A.; Jamison,
9, 487-498, 1990
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12913; PMID:1557383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prate prothrombin PMID:1557383
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acid; glycoprotein;
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Query Match

43.9%; His,

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Length

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predicted 2;

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coagulation factor VIIa (EC 3.4.21.21) - b C:Species: Bos primigenius taurus (cattle) C:Date: 21-May:1990 #sequence_revision 23-C:Accession: A31979; C20274
                                      R;Takeya, H.; Kawabata, S.; Nakagawa, Sakaya A.; Kawabata, S.; Nakagawa, 1988
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F;90-121/Domain: EGF homology <EG1>
F;109-167/Domain: EGF homology <EG2>
F;129-167/Domain: EGF homology <EG2>
F;129-167/Domain: EGF homology <EG2>
F;186-475/Product: coagulation factor X heavy chain #status predicted <HCH>
F;186-240/Domain: activation peptide #status predicted <APT>
F;241-475/Product: coagulation factor XB heavy chain #status experimental <AHC>
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C; Superfamily: coagulation factor X; EGF homology; Gla-domain homology; trypsin homology
C; Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
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R;Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.;
FEBS Lett. 283, 281-285, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Gallus gallus (chicken)
C;Date: 12-Feb-1993 #sequence_revision 07-Feb-1997 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coagulation
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A;Residues: 241-246,'X',248-251,'X',253-261 <GOT>
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A; Residues: 1-475 <SUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;241-468/Domain: trypsin homology <TRY>;46.47.54,56.59,60,65,66,69,72,75.79,Wodified site: gamma-carboxyglutamic acid (Glu);57-62,90-101,95-110,112-121,129-140,136-152,154-167,175-348,247-252,267-283,396-410,137-162,90-101,95-10,112-121,129-140,136-152,154-167,175-348,247-252,267-283,396-410,137-162,90-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100-10,100
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-40/Domain: propeptide #status predicted <PRO>
25-84/Domain: Gla domain homology <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Domain: signal sequence #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolation of factor Xa from chick nce number: S20380; MUID:92164779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANS-FLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWS 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANSGFLEELRKGNLERECVEEQCSYEEAFEALESPQDTDVFWAKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANSFLEEMKQGNIERECNEERCSKEEAREAFEDNEKTEEFWN 82
                                                                                                                                                                                                                                               factor VIIa (EC 3.4.21.21) - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . Similarity 42.: 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      catalyzes the proteolytic activation of prothrombin to thrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xa (EC 3.4.21.6) precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.7%;
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Its purification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pred. No. 8.5e-06;
6; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 86; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                             K.; Yamamichi,
                                                                                                                                                              23-Mar-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            embryo as the PMID:1537403
and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chicken
complete amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <S1G>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 475;
                                                                У.; мiyata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amniotic endoprotease responsit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gotoh, B.; Ogasawara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from chick embryo. Its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID: g222870
acid
                                                                                                                                                                  16-Jul-1999
                                                                        T.; Iwanaga,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;;
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sequence
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            F:1-51/Domain: Gla domain homology (fragment) <GI F:1-7/Domain: signal sequence (fragment) #status F:8-642/Product: plasma protein S #status predict F:87-120/Domain: EGF homology <FG1.
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A; Gene: PROS

plasma protein S; EGF homology; Gla domain homology; laminin

#status predicted
predicted <MAT>

<SIG>

ဂ

; Genetics:

A;Cross-references: EMBL:L31380
A;Experimental source: tissue type liver
A;Note: the source is designated as rhes

as rhesus monkey

A; Molecule type: mRNA

Residues: 1-642 <GRE>

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plasma protein S precursor, vitamin K of C; Species: Macaca mulatta (rhesus macaca C; Date: 19-Mar-1997 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;McMullen, B.A.; Fujikawa, K.; Kisiel, W. Biochem. Biophys. Res. Commun. 115, 8-14, 1983 A;Title: The occurrence of beta-hydroxyaspartic acid in the vitamin A;Reference number: A20274; MUID:83308813; PMID:6688526 A;Accession: C20274
                             Blochem. J. 305, 397-403, 1995
A;Title: Identification of candidate residues for interaction of A;Reference number: S53433; MUID:95134217; PMID:7832752
A;Accession: S53434
                                                                                                                                                       C; Accession: S53434
R; Greengard, J.S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;52/Binding site: carbohydrate (Ser) (covalent) #status experimental F;63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status e: F;145,203/Binding site: carbohydrate (Asn) (covalent) #status experimental F;152-153/Cleavage site: Arg-Ile (coagulation factor XIIa) #status experimental F;193,242,344/Active site: His, Asp, Ser #status predicted F;290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;153-387/Domain: trypsin homology <TRY>
F;6,7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxyglutamic acid (Glu) #sta
F;17-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: coagulation factor x; EGF homology; Gla domain homology; trypsin homol C;Keywords; beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu F;1-132/Product: coagulation factor VIIa light chain #status experimental <MA1> F;1-144/Domain: EGF domain homology (fragment) <GLA> F;50-81/Domain: EGF homology <EG1> F;91-127/Domain: EGF homology <EG2> F;53-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2> F;53-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         {\tt A; Description:} catalyzes the proteolytic activation of coagulation gulation factor IX in the presence of calcium and tissue factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood A; Reference number: A44556; MUID:89213999; PMID:3149637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A; Accession: A31979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Pathway: blood coagulation extrinsic pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Note: structure and location of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Contents: annotation
         A;Status: nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFW
                                                                                                                                                                                                                                                                                                                                                                                                                                             ANGFLEELLPGSLERECREELCSFEEAHEIFRNEERTRQFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                 precursor, vitamin K dependent -
mulatta (rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
   acid sequence not
                                                                                                                                                       Fernandez, J.A.; Radtke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A31979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 85; DB 1;
Pred. No. 9.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          covalently bound
         shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
not compared with conceptual translation
                                                                                                                                                          K.P.; Griffin,
                                                                                                                                                                                                                                                                               rhesus macaque (fragment)
                                                                                                                                                                                                                 #text_change 16-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 407;
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                                                                                                                                                       J.H.
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                                                                                                protein
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ta, T.;
                                                                                                S with
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A;Cross-references: GB:J02919
R;Ploos van Amstel, J.K.; van der Zanden, A
Thromb. Haemost. 58, 982-987, 1987
A;Title: Two genes homologous with human pr
A;Reference number: A60903; MUID:88178564;
                                               A; Molecule type: mRNA
A; Residues: 351-676 < PLO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N; Alternate r
C; Species: Hc
C; Date: 21-Se
                                                                                                    A; Accession: A60903
                                                                                                                                                                                                                                                        A;Residues:
                                                                                                                                                                                                                                                                                                                                                  A; Title: Molecular analysis of the gene fo A; Reference number: A35612; MUID:91084446;
                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 27-220, 'L', 222-262, 'H', 264-344, 'Y', 345-676 <LUN>
A; Residues: 27-220, 'L', 222-262, 'H', 264-344, 'Y', 345-676 <LUN>
A; Rosidues: GB: M14338; NID: g190448; PIDN: AAA60181.1; PA; Note: part of this sequence, including the amino end of the R; Edenbrandt, C.M.; Lundwall, A.; Wydro, R.; Stenflo, J.
Biochemistry 29, 7861-7868, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-10, P',12-25,'L',27-676 <HOS>
A;Cross-references: GB:M15036; NID:g190288; PIDN:AAA36479.1; PID:g190289
R;Lundwall, A.; Dackowski, W.; Cohen, E.; Shaffer, M.; Mahr, A.; Dahlback, Proc. Natl. Acad. Sci. U.S.A. 83, 6716-6720, 1986
A;Title: Isolation and sequence of the cDNA for human protein S, a regulatc A;Reference number: A23891; MUID:86313649; PMID:2944113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;HOSkins, J.; Norman, D.K.; Beckmann, R.J.; Long, G.L. Proc. Natl. Acad. Sci. U.S.A. 84, 349-353, 1987 A;Title: Cloning and characterization of human liver cDNA A;Reference number: A26157; MUID:87092407; PMID:3467362 A;Accession: A26157
                                                                                                                                                                                                                                                                                A; Molecule type:
                                                                                                                                                                                                                                                                                                A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                  A; Accession: A35612
                                                                                                                                                                                                                                                                                                                                                                               A; Title: Molecular analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F:171-207/Domain: EGF homology <EG3>
F:213-248/Domain: EGF homology <EG4>
F:281-633/Domain: sex hormone-binding globul
F:291-444/Domain: laminin G repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M57853; NID:g190547; PIDN:AAA60357.1; PID:g190549; GB:J02917 A;Note: the authors translated the codon TTT for residue 26 as Leu R;Ploos van Amstel, translated, P.H.; van der Logt, C.P.E.; Bertina, R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                뮹
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasma protein S precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: A25891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \;Residues: Î-25 <PL3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Title: Intron-exon organization of the active human protein S gene PSalpha and its;Reference number: A35611; MUID:91084445; PMID:2148111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: GB:J02918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title: Organization of the human protein S genes. Reference number: A35610; MUID:91084444; PMID:2148110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schmidel, D.K.; Tatro, A.V.; Phelps, L.G.; Tomczak, lochemistry 29, 7845-7852, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: A35611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Date: 21-Sep-1990 #sequence_revision 26-Jan-1996 #text_change 16-Jul-1999 Accession: A35610; A35611; A26157; A25891; A35612; A60903; S02424; S09519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                          van Amstel
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                                                                                                                                                                                                                                                   284-676 <EDE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-676 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          names: vitamin K-dependent protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
17; Conserv
tel, H.K.; van der Zanden, A.L.; Reitsma, P.H.; 186-190, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7853-7861, 1990
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38.68;
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                             for vitamin K dependent protein S
46; PMID:2148112
                                                                                                                    protein S cDNA
4; PMID:2895503
                                                                                                                                                                                           A.L.; Bakker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <LGR>
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                                                                                                                                            are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PID: g190449
                                                                                                                                                                                                                                                                                                                                                                                                                                                 mature
               Bertina,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                           P.H.;
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                                                                                                                                         chromosome
               R.M.
                                                                                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                         Bertina, R.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B.; Stenflo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of blood
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Search completed: May 16, Job time: 20 secs

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F;477,48,55,57,60,61,66,67,70,73,77/Modified site: gamma-carboxyglutamic acid (Glu)
F;58-63,88-113,121-134,126-143,145-154,161-175,171-184,186-199,205-217,212-226,228
F;111-112/Cleavage site: Arg-Ser (thrombin) #status predicted
F;136/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F;177,219,258/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GDB:120721; OMIM:176880
A;Map position: 3p11.1-3q11.2
A;Introns: 26/1; 78/3; 87/1; 116/1; 157/1; 201/1; 243/1; 283/3; 322/2; 385/3; 441/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Complex:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Description: a cofactor for activated protein C (EC 3.4.21.69); thrombin cleavage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;25-41/Domain: propeptide #status predicted <PRO>;26-85/Domain: Gla domain homology <GLA>
;42-676/Product: plasma protein S #status predictors: plasma protein 
                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                      Best
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205-241/Domain: EGF homology <EG3>
247-282/Domain: EGF homology <EG4>
                                                                                                                                                                                                                                                                                                                                    Query Match
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Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood coagulation;
1-24/Domain: signal sequence #status predicted <SIG>
           42
                                                                                                                                                                                                                                                                                 Local
                                                                                                1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
ANSLLEETKQGNLERECIEELCNKEEAREVFENDPETDYFYPKY
                                                                                                                                                                                                                                                                                                                                                                                                                                     .530/Binding site: carbohydrate (Asn) (covalent) #status
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17; Conser
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                                                                                                                                                                                                                                                                43.18; 38.68;
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Pred. No. 1.6e-05;
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85
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                             BLOSUM62
Gapop 10.0 , Gapext 0
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197
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 SwissProt_40:*
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 PRTC_HUMAN
PRTC_RABIT
PRTC_PIG
PRTC_PIG
PRTC_BOVIN
FA10_BOVIN
FA10_RABIT
FA7_HUMAN
TMG3_HUMAN
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Q28520
P07225
Q9bzd6
P00734
P81428
P98118
P70375
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P08709
O14668
P18292
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P07224
P53813
P00741
P00735
Q08761
                                                                                                                                                                                                                                                                                                                                                                                                                                                        P04070 homo sapien
P33587 mus musculu
P31394 rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
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7 bos taurus
6 macaca mula
5 homo sapien
6 homo sapien
6 tropidechis
6 cryctolagus
6 mus musculu
1 canis famil
7 mus musculu
1 dus musculu
1 bos taurus
3 rattus norv
1 bos taurus
                                                                                                                                                                                                                                                       2 homo sapien
7 homo sapien
8 oryctolagus
9 oryctolagus
9 homo sapien
8 homo sapien
2 rattus norv
1 mus musculu
5 gallus gall
                                                                                                                                                                                                                                                                                                                                                                                              l oryctolagus
2 sus scrofa
5 bos taurus
5 bos taurus
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;	45	44	43	42	41	40	39	38	37	36	<u>3</u> 5	34
:	47	47	47	47	48	48	48	49	50	52	65	65.5
;	23.9	23.9	23.9	23.9	24.4	24.4	24.4	24.9	25.4	26.4	33.0	33.2
;	1348	1343	554	244	1298	1235	422	1363	363	501	202	400
1	ب	<u>,_</u>	<b></b>	_	ب	_	ـــ	ب	<u>_</u>	۳	<u></u>	_
	VGR2 COTJA	VGR2_RAT	DHAB_SALTY	T2E5_ECOLI	VGR3_HUMAN	CYA4_TRYBB	SPM1_SCHPO	VGR3_MOUSE	ADK_TOXGO	MKC1_CANAL	TMG2_HUMAN	PRTZ_HUMAN
- 1	P52583	008775	P37450	P04390	P35916	026721	092398	P35917	Q9tvw2	P43068	014669	P22891
	coturnix co	rattus norv	salmonella	escherichia	homo sapien	trypanosoma	schizosacch	mus musculu	toxoplasma	candida alb		homo sapien

## ALIGNMENTS

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CARBOHYDRATE-LINKAGE SITE ASN-371.  MEDLING-90233094; PubMed=1694179;  Miletlich J.P., Broze G.J. Jr.;  "Beta protein C is not glycosylated at asparagine 329. The rate of translation may influence the frequency of usage at asparagine-X-cysteine sites.";  J. Biol. Chem. 265:11397-11404(1990).	Nickerson D.A.; Nickerson D.A.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. [5] SEQUENCE OF 106-461 FROM N.A. MEDLINE-84272714; PubMed-6589623; Foster D.C., Davie E.W.; "Characterization of a cDNA coding for human protein C."; Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).	of its messenger RNA, based upon the DNA sequence of liver cDNAs."; s Res. 13:5233-5247(1985).  M.A.  M.A.  Hoskins J.A., Long G.L., Crabtree G.R.; and organization of the human protein C gene."; Acad. Sci. U.S.A. 83:546-550(1986).  M.N.A.	11887; avie E.W.; the gene for human protein C."; 1. 82:4673-4677(1985). Santerre R.F., Plutzky J., Crab	LT 1 HUMAN STANDARD; PRT; 461 AA. PRTC_HUMAN PRTC_HUMAN PRTC_HUMAN PRTC_HUMAN PRTC_HUMAN PRTC_HUMAN PRTC_HUMAN PRTC_HUMAN PRTC_HUMAN PROV-1986 (Rel. 03, Created) Ol-NOV-1986 (Rel. 03, Created) Ol-NOV-1986 (Rel. 03, Created) PROV-1986 (Rel. 03, Created) PROC. PROC. Homo sapiens (Human) Bukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; NCBI_TaxID-9606;

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Fisher C.L., Greengaru u.s., "Models of the serine protease domain plasma factor activated protein C and Protein Sci. 3:588-599(1994).
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Sala N. (Cooper D.N.)
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mutations in the protein C gene.
Proc. Natl. Acad. Sci. U.S.A. 84
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domain of factor XII but not protein C.",
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VARIANT LEU-289.
MEDLINE=92380660;
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effects.";
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Reitsma P.H., Pool
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Leonardi A., Vicente
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MEDLINE-87204221;
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MEDLINE=97157472; PubMed=9003757;
Mather T., Oganessyan V., Hof P., Hub
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⊃ J. 15:6822-6831(1996).
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sma P.H., Poort S.R., Allaart C.F.,
spectrum of genetic defects in a pi
tomatic protein C deficiency type I
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                                                                                               ASP-418 (HONG
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2342; PubMed=8003977;
Greengard J.S., Grif
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H.J., Staempfli S
ente V., Mannucci
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PubMed=1347706;
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causing thrombosis.";
17:10513-10513(1989).
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PubMed=1511988

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Tsay W., Greengard J.S., Montgomery R.R., McF
Koerper M.A., Coughlin J., Griffin J.H.;
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                                                                                                                                                                                                causing type 2 protein
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                                                                                                                                                                                                                  MEDLINE=93271396; PubMed=8499568; Millar D.S., Grundy C.B., Bignell Kakkar V.V., Cooper D.N.; "A Gla domain mutation (Arg 15-->7
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Five novel mutations located in "Five novel mutations with
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mutation that
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Gandrille S., Vidaud M., Alach M., Alhenc-Gelas
Gouault-Hellman M., Toulon P., Fiessinger J.N.,
"Two novel mutations responsible for hereditary
                                                                    MEDLINE=94001606; PubMed=8398832;
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Bertina R.M.
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QF
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89:685-686(1992).
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Best Local Similarity 70.5%;
Matches 31; Conservative
                                           INTO A LIGHT CHAIN AND A HEAVY CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS STRONGLY PROMOTED BY THROMBOMODULIN.

-I- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
-I- TISSUE SPECIFICITY: DASMA; SYNTHESIZED IN THE LIVER.
-I- MISCELLANEOUS: CALCUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING THROMBOMODULIN COMPLEX.
-I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                      region of mammalian protein C.";
Br. J. Haematol. 86:590-600(1994).
Br. J. Haematol. 86:590-600(1994).
I. FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
I. CATALYTIC ACTIVITY: Degradation of blood coagulation
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01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vitamin-K dependent protein C precursor (EC 3)
(Autoprothrombin IIA) (Anticoagulant protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92316897; PubMed-1618739; Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.; "Isolation and characterization of a mouse protein C cDNA."; J. Blochem. 111:491-495(1992).
            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                               "Nucleotide structure and anticoagulant protein C.",
                                                                                                                                                                                                                                                                                                                                                                                                                        Jalbert L.R., Rosen E.D., Castellino F.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
                                                                                                                                                                                                                                                                                                                            Murakawa M., Okamura
                                                                                                                                                                                                                                                                                                                                      MEDLINE-94318474; PubMed-8043441;
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 274-434 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      Thromb.
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98152576; PubMed-9493582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
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                                                                                                                                                                                                                  and VIIIa.
SUBUNIT: S
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  Swiss Institute
Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                          characterization of the murine gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                  Lissens
  Institute.
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pred. No. 9.1e-20;
2; Mismatches 11
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Sciurognathi; Muridae,
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catalytic
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  PRINTS; PRO0722; CHYMOTRYPSIN.
PRINTS; PRO0701; GLABLOOD.
SMART; SM000179; EGF_LCA; 1.
SMART; SM00001; EGF_LIKe; 1.
SMART; SM00002; Tryp_SPc; 1.
SMART; SM000020; Tryp_SPc; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 2.
MOD_RES
ACT_SITE
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Pfam; PF00089; trypsin; 1.
Pfam; PF00594; gla; 1.
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InterPro; IPR000294; VitK_dep_GLA.
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InterPro; IPR001881;
InterPro; IPR002383;
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000561; EGF-like.
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MGI:97771; I
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PS00022;
PS01186;
PS01187;
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PS50240;
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TRYPSIN_HIS; 1.
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(BY SIMILARITY),
GAMMA-CARBOXYGLUTAMIC /
(BY SIMILARITY),
GAMMA-CARBOXYGLUTAMIC /
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PROTEIN C HEAVY CHAIN (I
ACTIVATION PEPTIDE (BY S
CLEAVAGE (BY THROMBIN)
CHARGE RELAY
CHARGE RELAY
CHARGE RELAY
BY SIMILARITY
BY SIMILARITY
BY SIMILARITY
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Query Match
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p31394;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence upda
15-JUN-2002 (Rel. 41, Last annotation up
Vitamin-K dependent protein C precursor
(Autoprothrombin IIA) (Anticoagulant pro-
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"The cDNA cloning and mRNA expression of rat protein C."
Biochim. Biophys. Acta 1131:329-332(1992).
-I- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE
REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS
IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
-I- CATALTIIC ACTIVITY: Degradation of blood coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Wistar; TISSUE-Liver; MEDLINE-92329550; PubMed-1627650;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING STREET IS RECECCEDED.
     European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
                                                                                                   SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                                                                                                   SITE IS NECESSARY FOR THE RECOGNITION THROMBIN-THROMBOMODULIN COMPLEX.
                                                                                                                                                                                                                                                                                                                                                      and VIIIa.
                 SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation suropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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IPR001314; Chymotrypsin.
IPR000561; EGF-like.
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IPR002383; GLA_blood.
IPR001254; Ser_protease_Try.
IPR000294; V1tK_dep_GLA.
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; GLA; 1.
; TYPP_SPC; 1.
; TYPP_SPC; 1.
10; ASX_HYDROXYL;
10; ASX_HYDROXYL;
10; EGF_1; 1.
86; EGF_2; 2.
87; EGF_CA; 1.
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TRYPSIN_HIS; 1.
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HYDROXYLATION (BY SIN
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CHARGE RELAY SYSTEM.
BY SIMILARITY.
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PROTEIN C HEAVY CHAIN (E
ACTIVATION PEPTIDE (BY S
CLEAVAGE (BY THROMBIN) (EGF-LIKE 1.
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GAMMA-CARBOXYGLUTAMIC
(BY SIMILARITY).
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CARBOHYD
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CARBOHYD
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-IT SISUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
-IP THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
-INISCELLANEOUS: CALCIUM ALSO BINDS, WITH "STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING SITE IS NECESSARY FOR THE RECOGNITION OF THE THROMBIN-THROMBOMODULIN COMPLEX.
-IS SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                       the European Bioinformatics Institute. Ther use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See For send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRTC_RABIT STANDARD; PRT; 458 AA. Q28661; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Vitamin-K dependent protein C precursor (EC 3.4.21.69) (Autoprothrombin IIA) (Anticoagulant protein C) (Blood factor XIV) (Fragment).
                                         EMBL; U49933; AAA92956.1; HSSP; P04070; 1PCU. MEROPS; S01.218; -.
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IPR000561;
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Pfam; PF00089; gla; 1.

SMART; SM00181; EGF; 2.

SMART; SM00069; GLA; 1.

SMART; SM00069; Tryp_SPC; 1.

PROSITE; PS00010; ASX_HYDROXYL; 1.

PROSITE; PS00010; ASX_HYDROXYL; 1.

PROSITE; PS01186; EGF_2; 2.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS001197; EGF_CA; 1.

PROSITE; PS001197; GLU_CARBOXYLATION; 1.

PROSITE; PS00134; TRYPSIN_DOM; 1.

PROSITE; PS00135; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_HIS; 1.
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  Similarity
26; Conser
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IPR001254;
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GAMMA-CARBOXYGLUTAMIC A
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GAMMA-CARBOXYGLUTAMIC A
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PROTEIN C LIGHT CHAIN (BY SIMILARITY).
PROTEIN C HEAVY CHAIN (BY SIMILARITY).
ACTIVATION PEPTIDE (BY SIMILARITY).
CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
EGF-LIKE 1.
  Pred. No. 5.70
; Mismatches
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GAMMA-CARBOXYGLUTAMIC
(BY SIMILARITY).
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GAMMA-CARBOXYGLUTAMIC
                                         Score 138;
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                                            Length 458;
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domains.";
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"Porcine factor V:
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombomodulin.

TISSUE SPECIFICITY: Plasma; synthesized in the liver.

PIM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.

MISCELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the GLA domain. This GLA-independent binding site is necessary for the recognition of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. Mol. Lif
FUNCTION:
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                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regulates blood coagulation by inactivating factors in the presence of calcium ions and phospholipids.
CATALYTIC ACTIVITY: Degradation of blood coagulation
                                                                                                                                                                                                                                                                                                    thrombin-thrombomodulin complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and VIIIa.
                                                                                                                                       AF191307;
P04070; 1
                        PF00008;
                                                                                                                            S01.
                                                                                                                                                                          an email to license@isb-sib.ch).
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                                                                                     IPR001314;
IPR000561;
                                                                                                               IPR000152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Life Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthesized as a single chain precursor, which ight chain and a heavy chain held together by a
                                                                                                                                     1PCU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fe Sci. 58:148–159(2001).
Protein C is a vitamin K-dependent
trypsin; 1. gla; 1.
                        EGF; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA cloning, gene mapping, f membrane binding sites and
                                  Ser_protease_Try.
VitK_dep_GLA.
                                                                                   Chymotrypsin
EGF-like.
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                                                            GLA_blood.
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Query Match Best Local Matches 2

Similarity

62.4%;

Score 123; DB 1; Pred. No. 2.2e-13;

Length 459

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SM00001; EGF_like;
SM00069; GLA; 1.
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Endothelial cell; Hydrolase;
     WW;
INTERCHAIN (BY SIMILA
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BY SIMILARITY,
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PROTEIN C HEAVY CHAIN
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ding; Vitamin K; Hydroxylation;
''' Hydrolase; Signal.
                                                                                                                   SIMILARITY).
     CRC64;
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21-JUL-1986
13-AUG-1987
                                                                                   Johnson A.E., Esmon N.L., Laue T.M., Esmon C.T.;

*Structural changes required for activation of protein C by Ca2+ binding to a high affinity site that does not con carboxyglutamic acid.*;

J. Biol. Chem. 258:554-5560(1983).

-I- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE P REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS V.

IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.

-I- CATALYTIC ACTIVITY: Degradation of blood coagulation and VIIIa.
                                                                                                                                                                                                                                                                                                MEDLINE-83007326; PubMed-6896877;
Stenflo J., Fernlund P.;
Stenflo J., Fernlund P.;
"Amino acid sequence of the heavy cha
J. Biol. Chem. 257:12180-12190(1982).
                                                                                                                                                                                                                                                                                                                                                                 Prakenberg T., Fernlund P., Ro
"Beta-hydroxyaspartic acid in
oron Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vitamin-K dependent protein C precursor (EC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood factor XIV) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                            Fernlund P., Stenflo J.;
"Amino acid sequence of the light chain
J. Biol. Chem. 257:12170-12179(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-85014826; PubMed-*091100;
Long G.L., Balagaje R.M., McGillivray R.T.A.;
"Cloning and sequencing of liver cDNA coding for
Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ce
Mavidae; Bovinae; Bos.
                                                                                                                                                                                            PROCESSING, AND CALCIUM-BINDING DATA MEDLINE-83213514; PubMed-6406503;
                                                                                                                                                                                                                           domainles protein C.";
J. Biol. Chem. 258:5548-5553(1983).
                                                                                                                                                                                                                                                         MEDLINE-83213513; PubMed-6304092; Esmon N.L., Debault L.E., Esmon C.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BOVIN
                                                                                                                                                                                                                                          "Proteolytic formation and properties
domainless protein C.":
                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 197-456
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-83169769; PubMed-6572939;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 40-194.
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SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVEI INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOCETHER BY A DISULFIDE BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN: THIS REACTION, WHICH CLEAVES AT THE SURFACE OF ENDOTHELIAL CELLS, IS STRONGLY PROMOTED BY THROMBOMODULIN.

TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.

PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
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1TE: PS00010; ASX_HYDROXYL; 1.
1TE: PS001186; EGF_2; 2.
1TE: PS01187; EGF_CA; 1.
1TE: PS00187; EGF_CA; 1.
1TE: PS00134; TRYPSIN_HS; FALSE_NE
1TE: PS00135; TRYPSIN_HS; FALSE_NE
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GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER APFINITY ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT SITE IS NECESSARY FOR THE RECOGNITION OF THE THROMBIN-THROMBOMODULIN COMPLEX.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS. or O BINDING

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Glycoprotein; Serine protease;
mic acid; Calcium-binding; Vitamin K; Hydroxylation;
epeat; Endothelial cell; Hydrolase; Signal.

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13-AUG-1987
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Bovidae; Bovinae;
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MEDLINE=76053069; Pu
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"The occurrence of beta-hydroxyaspartic acid
K-dependent blood coagulation zymogens.";
                                                                                                                                                                                                                                                                               MEDLINE=83308813; PubMed=6688526; MCMullen B.A., Fujikawa K., Kisiel W.;
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"Blood coagulation factor X mRNA encodes containing a prepro leader sequence."; Nucleic Acids Res. 12:4481-4492(1984).
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PubMed=8243461;
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Res. Commun. 115:8-14(1983).
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"The relative orientation of Gla and EGF domains in c
factor X is altered by Ca2+ binding to the first EGF
combined NMR-small angle X-ray scattering study.";
Biochemistry 35:11547-11559(1996).
-I- FUNCTION: Factor Xa is a vitamin K-dependent glyo
converts prothrombin to thrombin in the presence
                                                                                                                                                                                                     "How an epidermal growth factor (EGF)-like do resolution NMR structure of the calcium form like domain in coagulation factor X.";
J. Biol. Chem. 267:19642-19649(1992).
                                                                                                                                                                                                                                                                                                                 "Three-dimensional structure of the apo
EGF-like module of blood coagulation fac
spectroscopy and simulated folding.";
Biochemistry 31:5974-5983(1992).
                                                                                                                                                     MEDLINE=96387194; PubMed=8794734; Sunnerhagen M., Olah G.A., Stenflo
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"Localization of the structural difference between bovine blood "Localization factors XI and X2 to tyrosine 18 in the activation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=76053121; PubMed=1059122; Fujikawa K., Titani K., Davie E.W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an serine proteases.";
11:4899-4903(1972).
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                                                                                                                                                                                                                                                              PubMed=1527084;
PubMed=1527084;
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MEROPS; SO1.216; ...

GlycoSuitedB; P00743; ...
GlycoSuitedB; P00743; ...
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000314; Chymotrypsin.
InterPro; IPR000742; EGF-21.
InterPro; IPR000742; GEF-Ca.
InterPro; IPR001881; EGF-Ca.
InterPro; IPR001234; Ser_protease_Try.
InterPro; IPR00234; YitK_dep_GLA.
InterPro; IPR000294; YitK_dep_GLA.
Pfam; PF00008; EGF; 2.
Pfam; PF00009; LTYPSIN; 1.
Pfam; PF00594; 91a; 1.
Pfam; PF00594; 91a; 1.
Pfam; PF00594; 91a; 1.
PAMRT; SM00101; GLABLOOD.
SMART; SM00101; EGF_11ke; 1.
SMART; SM00006; GLA; 1.
SMART; SM00006; GLA; 1.
SMART; SM00006; GLA; 1.
SMART; SM00006; GLA; 1.
PROSITE; PS00116; ASX_HYDROXYL; 1.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00134; TRYPSIN_DOW; 1.
PROSITE; PS00135; TRYPSIN_DOW; 1.
PROSITE; PS00135; TRYPSIN_DSF; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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PIR; A00925; EXBO.
PDB; 1APO; 31-JAN-94.
PDB; 1CCF; 31-MAY-94.
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PTM: N- AND O-GLYCOSYLATED.

PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE PINTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTHINSIC PATHWAY).

INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTHINSIC PATHWAY).

MISCELLAMEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
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PTM: THE VITAMIN K-DEPENDENT,
GLUTAMIC ACID RESIDUES ALLOWS
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tamic acid; HydroxyLation; Calcium-binding; Vitamin K;
EGF-like domain; Repeat; Sulfation; 3D-structure.
23
 122
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; EGF_Ca.
; GLA_blood.
; Ser_protease_Try.
; V1tK_dep_GLA.
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EGF-LIKE 1, CALCIUM-BIN
EGF-LIKE 2.
SERINE PROTEASE.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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GAMMA-CARBOXYGLUTAMIC A
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FACTOR X HEAVY CHAIN.
ACTIVATION REPTIDE.
ACTIVATED FACTOR XA, HEAVY CHAIN.
MAY BE REMOVED BUT IS NOT NECESSARY FOR
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SEQUENCE OF TISSUE-Live MEDLINE-842 Leytus S.P.	MEDLINE-83257207; PubMed MCMullen B.A., Fujikawa K.W. E.Y., Weinstein B.; "Complete amino acid seq coagulation factor x: ev beta-hydroxyaspartic acid Biochemistry 22:2875-288	SEQUENCE OF TISSUE-Liver MEDLINE-8622 Kaul R.K., H "Isolation a cDNA."; Gene 41:311-	ochemist    QUENCE O  DLINE=85  ng M.R.,  haracter  ood coag  oc. Natl	SEQUENCE FROM MEDLINE-870266 Leytus S.P., F "Gene for huma organization i profession of the second s	EQUE EDLI essi Clon Clon uman	UMAN A10_HUMA 00742; Q 00742; Q 1-JUL-19 1-OCT-19 5-JUN-20 0agulati 10. Sapi ukaryota ukaryota ukaryota cammalia; CBI_TaxI	y Ma Loc hes 1	MOD_RES MOD_RES MOD_RES MOD_RES
115-488 r; 22026; P	41-1/9. 41-1/9. 57207; pujli A., Fujli einstein mino acin factor yasparti y 22:287	F 19-488 FRC /er; 3221713; Pubw Hildebrand h and charact [1-314(1986)]	25:51 13-481 6545; ay C:1 ation ation acad.	w = 0 O Z	NCE FROM N.A. NE-91216473; Pubm er T.L., Pittman ing and expression coagulation fact 99:291-294(1991).	"": JEES A	tch 57.9%; Score 114; DB 1; L al Similarity 45.5%; Pred. No. 8.6e-12; 20; Conservative 8; Mismatches 16; ANSFLXXLROGSLLXXXCIXXICDFXXAKXIFEDVDDTLAFWSKH       ::  :      ::  !	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
M N.	K.,  equen  equen  oride  orid.  B84(1	+ I Z	098-5102(1986).  B FROM N.A.  PubMed=2582420 W., McGillivray of an almost f factor X."; Sci. U.S.A. 82	.A. 0; PubMed=376 ster D.C., Ku factor X: a essentially	PubMed=1902434 tman D.D., Long ession in COS-1 factor X.";	rea asi asi asi asi	57.9%; lty 45.5%; servative servative   SSLXRXCIXXICE  :     :	665 650 650
E. A	l67; lsiel of th e for	.A. 3011603; Roberts S zation of	, R. ull	8336; rachi blood ident	102434; Long G.L COS-1 cel	PRT; ) quence notati r (EC r (EC Crani	Score 1 Pred. N B; Misn DFXXAKXIE  : :  SLEEAREVE	ע כו כו כו
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98283982; PubMed=9618463; Kamata K., Kawamoto H., Honma T.,
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MEDLINE-90128299; Pubmed-2612918;

Jagadeeswaran P., Reddy S.V., Rao K.J.,

"Cloning and characterization of the 5'
encoding human factor X.";

Gene 84:517-519(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification of O-linked oligosaccharide chains in the activation peptides of blood coagulation factor X. The role of the carbohydrate moleties in the activation of factor X.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structural basis for chemical inhibition of human blood coagulation factor Xa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              x-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Padmanabhan
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EDLINE-93360277; PubMed-8355279;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting.

CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then Arg-|-Ile bonds in prothrombin to form thrombin.

SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OF
                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                       PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY). SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI: SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                      A00924; EXHU.
A25853; A25853.
A24478; A24478.
                                                                                                                                                                                                        ; K03194; AAA52490.1;
; M57285; AAA52421.1;
; L29433; AAA52764.1;
; L00390; AAA52764.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: N- AND O-GLYCOSYLATED.
PTM: THE ACTIVATION PEPTIDE IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: Plasma; synthesized in the liver PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MORE DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation
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SMART; SM00179; EGF_CA; 1.
SMART; SM00001; EGF_like;
                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00594;
                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00089;
                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00008;
                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00010;
                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 227600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlycoSuiteDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS; S01.216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HGNC:3528; F10.
                                                                                                                                                                                                                                                                         Zymogen; EGF-like
                                                                                                                                                                                                                                                                                                                                              PS00022;
                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR002383; GLA_blood.
IPR001254; Ser_protease_Try.
IPR000294; VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000152; Asx_hydroxyl IPR001314; Chymotrypsin IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR00188
276
322
419
90
95
112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-99
                                                                                                     79
103
                                                               231
                                                                                                                       01; EGF_like; 1.
69; GLA; 1.
20; Tryp_SPc; 1.
20; Tryp_SPc; 1.
00010; ASZ_HYDROXYL;
00022; EGF_1; 1.
1186; EGF_2; 2.
1186; EGF_2; 2.
                                                                                                                                                                                                                                                                                       Hydrolase; Serine protease; Plasma; Blood
                                                                                                                                                                                                                                                                                                                                                                                                            gla;
                                                                                                                                                                                                                                                                                 Lutamic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P00742;
                                                                                                                                                                                                                                                                                                                                                                                                                   trypsin; 1.
                                                                                                                                                                                                                                                                                                TRYPSIN_DOM; 1.
TRYPSIN_HIS; 1.
TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                     CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                        GLU_CARBOXYLATION;
 276
322
419
101
110
121
140
                                                              231
                                                                                                                        7566666647
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGF_Ca.
                                                                                                                                                                                                                                                                                 acid;
                                                                                                                                                                                                                                                                       d; Hydroxylation; Calcium-binding;
domain; Repeat; 3D-structure.
                                       CHARGE
CHARGE
                                                                           O-LINKED (GALNAC. .
O-LINKED (GALNAC. .
N-LINKED (GLCNAC. .
                                                      /FTId-CAR_000012.
N-LINKED (GLCNAC. .
/FTId-CAR_000013.
                                                                                                             GAMMA-CARBOXYGLUTAMIC GAMMA-CARBOXYGLUTAMIC
                                                                                                                              GAMMA-CARBOXYGLUTAMIC GAMMA-CARBOXYGLUTAMIC
                                                                                                                                                    GAMMA-CARBOXYGLUTAMIC
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                                                                                                                                                                                   GAMMA-CARBOXYGLUTAMIC GAMMA-CARBOXYGLUTAMIC
                                                                                                                                                                                                          ACTIVATION PEPTIDE:
ACTIVATED FACTOR XA, HEAVY CHAIN.
EGF-LIKE 1, CALCIUM-BINDING (POTH
EGF-LIKE 2.
                                                                                                       HYDROXYLATION.
                                                                                                                                             GAMMA-CARBOXYGLUTAMIC
                                                                                                                                                             GAMMA-CARBOXYGLUTAMIC
                                                                                                                                                                                                    SERINE PROTEASE
                                                                                                                                                                                                                                          FACTOR X LIGHT CHAIN.
                                                                                                                                                                                                                                                                  POTENTIAL.
                              E RELAY SYSTEM.
E RELAY SYSTEM.
                                                                                                             ACID.
                                                                                                                                                                                                                                                                               coagulation;
ing; Vitamin
                                                                                                                                                                                                                  (POTENTIAL).
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55.8%;

Score 110;

DB 1;

Length 488;

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TRESULT OF GRANDER HERE OF GRA
RESULT 10
FA10_RABIT
ID FA10_RABIT
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Matches
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Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins expressed broadly in fetal and adult tissues."; Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00594; gla; 1.
PRINTS; PR00001; GLABL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF326350
HSSP; P00740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Spinal cord;
MEDLINE-21117044; PubMed-11171957;
MURAN J.D., Hartis J.E., Xie L., Davie E.W.;
"Identification of two novel transmembrane ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TMG3_HUMAN
Q9BZD7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAMOH
                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00069; GLA; 1.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gamma-carboxyglutamic acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002383; GLA_blood.
InterPro; IPR000294; V1tK_dep_GLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5-JUN-2002
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                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: Expressed in brain, lung, kidney and heart. PTM: Gla residues are produced after subsequent posttranslational modifications of glutamic acid by a vitamin K-dependent gamma-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carboxylase.
                                                                                                                                                         ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFW 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANSFLEEMKKGHLERECMEETCSYEEAREVFEDSDKTNEFWNKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                             ANEFLEELROGTIERECMEEICSYEEVKEVFENKEKTMEFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF326350; AAK00955.1; -.
                                                                                                                                                                                                                         18; Conservative
                                                                                                                                                                                                                                                                                                                     20
79
102
23
231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ilarity 43.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1CFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gamma-carboxyglutamic acid protein 3 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD
     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLABLOOD.
                                                                                                                                                                                                                                                                                                              78
101
231
60
25848
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                                                                                                                                                                                                                                              54.3%;
43.9%;
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                                                                                                                                                                                                                         .,
                                                                                                                                                                                                                                              Score 107;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC
     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                        8A373E4848490D81
                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231
     490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                DB 1;
.9e-11;
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     ₹
                                                                                                                                                                                                                            15;
                                                                                                                             60
                                                                                                                                                                                                                                                                     Length 231;
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       A COUNTY AND A COU
                                                                       SMART; SM00179; EGF_CA; 1.

SMART; SM00001; EGF_Like; 1.

SMART; SM00000; GLA; 1.

SMART; SM00000; Tryp_SPC; 1.

PROSITE; PS00010; ASX_HYDROXYL; 1.

PROSITE; PS00012; EGF_1; 1.

PROSITE; PS01186; EGF_2; 2.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS011187; EGF_CA; 1.

PROSITE; PS011187; EGF_CA; 1.

PROSITE; PS011187; EGF_CA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                019045;
15-DEC-1998
15-DEC-1998
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <del>-</del> -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-97256311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                        PRINTS; PR00722; CHYMOTRYP. PRINTS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY).

MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY ANOTHER SITE, BEYOND THE GLA DOMAIN.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting.

CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-Thr and then Arg-1-Ile bonds in prothrombin to form thrombin.

SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MORE DISULFIDE BONDS.
PTM: THE VITAMIN K-DEPENDENT,
GLUTAMIC ACID RESIDUES ALLOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CALCIUM (BY SIMILARITY).

PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).

PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF003200;
P00742; 1
                                                                                                                                                                                                                                                                                                                                                                         PF00594; gla;
                                                                                                                                                                                                                                                                                                                                                                                                  PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Res. 85:503-514(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR000152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR00188
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(Rel. 37, Last sequence update)
(Rel. 41, Last annotation update)
The procursor (EC 3.4.21.6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cuniculus (Rabbit).
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
       Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THCG.
                                                                                                                                                                                                                                                                                                                                                                                                                            EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB62542.1;
                                                                                                                                                                                                                                                                                                                                                    CHYMOTRYPSIN
                              TRYPSIN_HIS;
TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=9101642;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chymotrypsin
EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Asx_hydroxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                Ser_protease_Try.
VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLA_blood
       Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .'
     protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENZYMATIC CARBOXYLATION THE MODIFIED PROTEIN TO
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DNA for rabbit factor X.";
       Plasma;
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       Blood
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       coagulation;
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Query Match
Best Local
                                                                                                                                                                                                                                           Matches
                                                                                                                   _RABIT
                  FA7_RABIT STANDARD; PRT; 444 AA. P98139; P79224; 01-FEB-1996 (Rel. 33, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Coagulation factor VII precursor (EC 3.4.21.21) (Serum
                                                                                                                                                                                                                                                                                                                                                                                            DISULFID DISULFID
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Signal; Zymogen; EGF-:
SIGNAL 1 20
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                                                                                                                                                                                                                                         Similarity
19; Conserv
         accelerator).
                                                                                                                                                                                                                                                                                                   490
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274
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417
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                                                                                                                                                                                                                                                                                                   AA;
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402
441
187
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                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             i; Hydroxylation; Calcium-binding;
domain; Repeat.
                                                                                                                                                                                                                                                                                                        CHARGE RELAY SYSTEM.

CHARGE RELAY SYSTEM.

CHARGE RELAY SYSTEM.

BY SIMILARITY.

BY SIMILARIT
                                                                                                                                                                                                                                       9;
                                                                                                                                                                                                                                                  Score 103; DB 1;
Pred. No. 6.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAMMA-CARBOXYGLUTAMIC SIMILARITY).
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GAMMA-CARBOXYGLUTAMIC
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY)
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GAMMA-CARBOXYGLUTAMIC
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ACTIVATED FACTOR XA, HEAVY CHAIN
EGF-LIKE 1, CALCIUM BINDING (POTI
EGF-LIKE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FACTOR X LIGHT CHAIN.
                                                                                                                                                                                                                                                                                                  3A39FA85AF2A6D11 CRC64;
                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat.
                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                 Length 490;
                                                                                                                                                                           84
                                                                                                                                                                                                        44
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                             ) (POTENTIAL).
) (POTENTIAL).
) (POTENTIAL).
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                    prothrombin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vitamin
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>~</u>
                                                                                                                                                                                                                                    0;
      PROSITE; PS00010; P
PROSITE; PS00022; E
PROSITE; PS01186; E
PROSITE; PS001187; E
PROSITE; PS00011; G
PROSITE; PS00240; T
PROSITE; PS00134; T
PROSITE; PS00134; T
                                                                                                                                                                                                                            Pfam; PF00008; EGF; 2.
Pfam; PF00089; trypsin; 1.
Pfam; PF00594; gla; 1.
                                                                                                                                                                                                                                                                                             InterPro;
InterPro;
                                                                                                                                          SMART;
                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                                                       InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U77477; AAB37326.1; HSSP; P08709; 1FAK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruiz S.R., Biajchman M.A., Clarke B.J.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.

FUNCTION: CIRCULARES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII
CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA,
THROMBIN BY MINOR PROTECLYSIS. IN THE PRESENCE OF TISSUE FACTOR
AND CALCIUM IONS, FACTOR VIIA THEN CONVERT FACTOR X TO FACTOR X
BY LIMITED PROTECLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX
FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
    Hydrolase;
                                                                                                                                                          SMART;
                                                                                                                                                                                       SMART;
                                                                                                                                                                                                      PRINTS;
                                                                                                                                                                                                                     PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F7.
Oryctolagus cuniculus (Rabbit).
Oryctolagus cuniculus (Rabbit).
Pularvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93190306; PubMed=83833365;
Brothers A.B., Clarke B.J., Sheffield W.P.
"Complete nucleotide sequence of the cDNA
                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete nucleotide factor VII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVISION TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thromb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY A DISULFIDE BOND (BY SIMILARITY).

IT TISSUE SPECIFICITY: PLASMA.

IT THE VITAMIN K-DEPENDENT, ENZYMATIC CA
GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED
CALCIUM (BY SIMILARITY).

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1

SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        form factor Xa.
SUBUNIT: HETERODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a sen the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                     ; PR00001;
SM00179; E
                                                                                                                                          SM00020;
                                                                                                                                                          SM00069;
                                                                                                                                                                        SM0000
                                                                                                                                                                                                                                                                                                                                                                                                     S01
                                                                                                                                                                                                                                                                                IPR000294;
                                                                                                                                                                                                                                                                                             IPR002383;
IPR001254;
                                                                                                                                                                                                                                                                                                                           IPR00188:
                                                                                                                                                                                                                                                                                                                                         IPR000742;
                                                                                                                                                                                                                                                                                                                                                                       IPR001314;
                                                                                                                                                                                                                                                                                                                                                         IPR000561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          395
                                                                                ; GLA; 1.
; Tryp_SPc; 1.
j10; ASX_HYDROXYL; j10; ASX_HYDROXYL; j22; EGF_1; 1.
186; EGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suppl.
                                                                                                                                                                  L; GLABLOOD.
; EGF_CA; 1.
; EGF_like; ]
                                                                                                                                                                                                                     CHYMOTRYPSIN
                               TRYPSIN_DOM; TRYPSIN_HIS;
                                                             EGF_CA; 1.
GLU_CARBOXYLATION;
                  TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                       52; Asx_hydroxyl
L4; Chymotrypsin
51; EGF-like.
                                                                                                                                                                                                                                                                                                          EGF_Ca.
GLA_blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69:231-238(1993).
                                                                                                                                                                                                                                                                                                                                         EGF_
                                                                                                                                                                                                                                                                               VitK_dep_GLA.
                                                                                                                                                                                                                                                                                            Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolyzes one Arg-|-Ile
    Blood
 coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENZYMATIC CAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN AND
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rabbit coagulation
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Glycoprotein;
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RESULT FA7\_RAB ID FA AC P9 DT 01 DT 15 DT 15 DE CC

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AND LYS-445

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RESULTION
RATALIUMAN
FA7_HUMAN
ID FA7_HUMAN
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STANUANCE
AC P007/09; 014/339;
AC P007/09; 014/339;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Se
Coagulation accelerator) (Eptacog alfa).
     RESULT
FA7_HUM
ID FA7
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PROPEP
TISSUE-Liver;
MEDLINE-86205965; PubMed-3486420;
Hagen F.S., Gray C.L., O'Hara P.J., Gray Colling and Markey M.Y.,
                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
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39
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49011
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Primates;
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BY SIMILARITY.

BY
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5; Mismatches
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                                                                                                     Craniata; V
Catarrhini;
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Y SIMILARITY .
Y SIMILARITY .
       Grant F.J., S
Y., Kisiel W.,
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1.3e-09;
17;
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1; Hominidae;
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                    Saari G
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        Kurachi K.
                                                                                                                  Euteleostomi;
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) (BY SIMILARITY)
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        STRUCTURE OF CARBOHYDRATE ON SER-112.

MEDLINE-90062160; PubMed-2511201;

Nishimura H., Kawabata S., Kisiel W., Hase S., J
Shimonishi Y., Iwanaga S.;

"Identification of a disaccharide (Xyl-Glc) and
"Identification of a disaccharide (Xyl-Glc) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bjoern S., Foster D.C., Thim L., Wiberg F.C., Christensen N. Komiyama Y., Pedersen A.H., Kisiel W.; "Human plasma and recombinant factor VII. Characterization glycosylations at serine residues 52 and 60 and effects of directed mutagenesis of serine 52 to alanine."; J. Biol. Chem. 266:11051-11057(1991).
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MEDILINE-89088153; PubMed=3264725;
Thim L., Bjoern S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,
Pedersen A.H., Hedner U.;
Pamino acid sequence and posttranslational modifications of human
"Amino acid sequence and posttranslational modifications of cells.";
                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS)
MEDLINE-99126538; PubMed-9925787;
Zhang E., St Charles R., Tulinsky A.;
"Structure of extracellular tissue fainhibited with a BPTI mutant.";
                                                                                                                                                                                                                              MEDLINE=96175641; PubMed=8598903;
Banner D.W., D'Arcy A., Chene C., Winkler
Konigsberg W.H., Nemreson Y., Kirchhofer
"The crystal structure of the complex of
VIIa with soluble tissue factor.";
                                                                                                                                                                                                                                                                                                                           STRUCTURE OF CARBOHYDRATE ON SER-112.

MEDLINE-91344709; PubMed-2129367;

Twanaga S., Nishimura H., Kawabata S., Kisiel W.,

"A new trisaccharide sugar chain linked to a serir
first EGF-like domain of clotting factors VII and
Adv. Exp. Med. Biol. 281:121-131(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                              (Xy12-Glc) O-glycosidically linked to a serin epidermal growth factor-like domain of human protein Z and bowline protein Z ; J. Biol. Chem. 264:20320-20325(1989).
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MEDLINE-91250411; Pubmed-1904059;
Bjoern S., Foster D.C., Thim L.,
Komiyama Y., Pedersen A.H., Kisie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rieder M.J., Armel T.Z., Poel C.L., Toth E.J., Yi Submitted (JAN-2002) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochemistry
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"Nucleotide
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                                              Drakenberg
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                                                             Muranyi A., Finn
                                                                          MEDLINE-98367502;
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"Characterization
                     "Solution structure factor VII.";
                                                                                                                                                                                                                  Nature
                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                  -RAY CRYSTALLOGRAPHY (2.0
                                                                                                                                                                                                                  ith soluble tissue 380:41-46(1996).
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                                                                                                                    Biol.
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.J., Armel T.Z., Carrington D.P., Chung M.,
., Toth E.J., Yi Q., Nickerson D.A.;
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                                                             В.Е.,
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PubMed=9692950;
Cinpert G.P.,
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A. 83:2412-2416(1986).
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bernardi F., Castaman G., Pinotti M.,
Lunghi B., Rodeghiero F., Marchetti G.
"Mutation pattern in clinically asympt
deficiency.";
                                                                                             Arbini A.A., Mannucci P.M., "A Thr359Met mutation in fac deficiency causes defective Blood 87:5085-5094(1996).
                                                                                                                                                                                                        "Factor VII Mie: homozygous an amino acid substitution catalytic domain.";
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                                                                                                                                                    VARIANT MET-419. 
MEDLINE=96247510; PubMed=8652821;
                                                                                                                                                                                                                                                                Ohiwa M.
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                                                                                                                                                                                                                                                                                                                                                                                                                           *Roberts H.R., Blajchman M., Monrc
*Severe factor VII deficiency cau
cleavage site for activation and
plood 83:3524-3535(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Detection of missense mutations by single-strand conformatipolymorphism (SSCP) analysis in five dysfunctional variants coagulation factor VII.";
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                                                       MEDLINE=97001216; . PubMed=8844208
                                                                      VARIANTS W-283;
                                                                                                                                                                                                                                                               MEDLINE-95064662;
Ohiwa M., Hayashi
                                                                                                                                                                                                                                                                                                                                                           Bernardi F., Castaman G., I
Rodeghiero F., Marchetti G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takamiya O., Kemball-Cook G., Marin D.M.A., von Felten A., Meili E., Hahn I., Prangnell Tuddenham E.G.D., McVey J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94061028;
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VARIANT GLN-364
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92340074; PubMed=1634227;
                                                                      K-325; V-358;
                                                                                                                                                                                                                                    homozygous
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T., Wada H., Minamikawa
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aman G., Redaelli
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                                       Ferraresi P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                           MEDLINE 9/30-77,
Kulman J.D., Harris J.E., Haldeman B.A., Davie E.T.,
Kulman J.D., Harris J.E., Haldeman B.A., Davie E.T.,
Primary structure and tissue distribution of two novel prol
gamma-carboxyglutamic acid proteins.";
Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
-!- TISSUE SPECIFICITY: Highly expressed in the spinal cord.
-!- TISSUE SPECIFICITY: Highly expressed in the spinal cord.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zaizov R., Seligsom. Probably ancient is a common, probably ancient is a common and Iranian Jews. deficiency in Moroccan and Iranian Jews. Haemost. 76:283-291(1996).
                                                                                                  MEDLINE=97404347; Pu
Kulman J.D., Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hum.
                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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014668;
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                                                                                                                               SEQUENCE FROM
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                                                                                                                                                                                                           PRRG1 OR
                                                                                                                                                                                                                                  rich Gla
                                                                                                                                                                                                                                                 Transmembrane
                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ++
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                                                                                                                                                                                               HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor VII gene.";
Hum. Mutat. Suppl. 1:S189-S191(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mishinder C., Scerri C., Galdies R., "Two new missense mutations (P134T a factor vit zono "
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                                                                                                                                                                                                                                                                                                                                                                               61 ANAFLEELRPGSLERECKEEQCSFEEAREIFKDAERTKLFW
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, THEOMBIN BY MINOR PROTEDLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR AND CALCIUM FOR FACTOR VIIA THEN CONVERTS FACTOR IN THE PRESENCE OF TISSUE FACTOR IX FACTOR IX IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.

CATALTIC ACTIVITY: Hydrolyzes one Arg-!-ILe bond in factor X to
                    PTM: Gla residues are produced modifications of glutamic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               produced by alternative splic
TISSUE SPECIFICITY: PLASMA.
PTM: THE VITAMIN K-DEPENDENT,
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SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND
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protein 1) (Proline-rich gamma-carboxyglutamic acid
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O., Korostishevsky
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coagulation
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RESULT 14
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Matches 17
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01-NOV-1990
15-JUN-2002
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DOMAIN
                               MEDLINE-92212913; pubMed-1557383;
Banfield D.K., Macgillivray R.T.;
"Partial characterization of vertebrate prothrombin cDNAs:
"Partial characterization of vertebrate prothrombin cDNAs:
"partial characterization of vertebrate prothrombin from nine different species.";
Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
-I- FUNCTION: THROMBIN AND ACTIVATES FACTORS V, VII, VIII, XIII, AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
-I- CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-Gly; activates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
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InterPro; IPR000294; V1tK_dep_GLA.
Pfam; PF00594; gla; 1.
PRINTS; PR00001; GLABLOOD.
SMART; SM00069; GLA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF009242; AAB67070.1; -. HSSP; P00740; 1CFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entitles requires a license agreement (See http://www.isb-sib.ch/announce/
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modified and this statement is not removed.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Prothrombin
                                                                                                                                                                                                            SEQUENCE OF 383-617
                                                                                                                                                                                                                                        Dihanich M., Monard D.;
"CDNA sequence of rat prothrombin.";
Nucleic Acids Res. 18:4251-4251(1990).
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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    fibrinogen to fibrin and releases fibrin PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES,
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17; Conservative
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Metazoa; Chor
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(Rel. 16, Last sequence update)
(Rel. 41, Last annotation update)
precursor (EC 3.4.21.5).
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Rodentia;
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GLA-RICH.
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    fibrinopeptide A and B.
SIDUES, WHICH BIND CALCIUM IONS
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RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY CHARGED PHOSPHOLIPID SURFACE, WHICH IS OF PROTHROMBIN TO THROMBIN. ESSENTIAL FOR THE CONVERSION

MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A PHOSPHOLIPID MEMBRANE THAT BINDS THE ANINO END OF PROTHROMBIN & FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES THE ACTIVATION PEPPIDE & CLEAVES THE REMAINING PART INTO LIGHT & HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR VITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF

FRAGMENT (FRAGMENT 1)
BY FACTOR XA.
- SIMILARITY: BELONGS TO
- SIMILARITY: CONTAINS 2 MISCELLANEOUS: THROMBIN FRAGMENT (FRAGMENT 1) OF Ş, CAN THE ITSELF CLEAVE THE AMINO TERMINAL PROTHROMBIN, PRIOR ö ITS ACTIVATION

BELONGS TO CONTAINS 2 PEPTIDASE FAMILY KRINGLE DOMAINS. S1

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SMART; SM00020; Tryp\_SPc; 1.

PROSITE; PS00011; GLU\_CARBXYLATION; 1

PROSITE; PS00021; KRINGLE\_1; 2.

PROSITE; PS50070; KRINGLE\_2; 2.

PROSITE; PS50240; TRYPSIN\_DOW; 1.

PROSITE; PS00134; TRYPSIN\_HIS; 1.

PROSITE; PS00135; TRYPSIN\_HIS; 1. PRINTS; PR00722; C PRINTS; PR00001; C PRINTS; PR00018; F PRINTS; PR01505; F ProDom; PD000395; Kringle; SMART; SM00069; GLA; 1. SMART; SM00130; KR; 2. SMART; SM00020; Tryp\_SPc; EMBL; X52835; CAA37017.1; -. EMBL; M81397; AAA42240.1; -. PIR; S10511; S10511. PF00089; coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat; in K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Livelase; Serine protease; Kringle; Signal. PF00051; P00734; IPR003966; Prothrombin.
IPR001254; Ser\_protease\_Try.
IPR000294; VitK\_dep\_GLA. IPR001314; Chymotrypsin.
IPR002383; GLA\_blood.
IPR000001; Kringle.
IPR003966; Prothrombin. luvs gla; kringle; trypsin; PROTHROMBIN GLABLOOD. protease; 43 617 200 323 359 617 187 187 292 201 201 324 458 KRINGLE CHYMOTRY PSIN. N SERINE PROTEASE.
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Best Local :
Matches 1:
           nine different species.",

Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).

-! FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERT FIBRINGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII, AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.

-!- CATALYTIC ACTIVITY: Preferential Cleavage: Arg-|-Gly; activates
                                                                                                      Banfield D.K., Macgillivray R.T.;
"Partial characterization of vertebrate prothrombin amplification and sequence analysis of the B chain c
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MEDLINE-91025551; PubMed-2222810;
Friezner Degen S.J., Schaffer L.A.,
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-NOV-1990 (Rel. 16,
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Fitzgibbon J.J., Pai J.-A., Chapman V.
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                     PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS, RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION OF PROTHROMBIN TO THROMBIN IS ACTIVATED ON THE SURFACE OF A PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN 6 PROTHROMBIN TO THE SURFACE OF A PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN 6 PACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT & HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR VITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF THROMBIN.
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MISCELLANEOUS: THROMBIN CAN ITSELF CLEAN FRACKENT (FRAGMENT 1) OF THE PROTHROMBIN BY EACTOR XA.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: CONTAINS 2 KRINGLE DOMAINS. THROMBIN CAN ITSELF CLEAVE MENT 1) OF THE PROTHROMBIN, S1. PRIOR THE AMINO TERMINAL TO ITS ACTIVATION

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PROSITE; PS00011; PROSITE; PS00021; PROSITE; PS50070; PROSITE; PS50240; PROSITE; PS00134; PROSITE; PS00135; DOMAIN
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InterPro; IPR000294; VitK\_dep\_GLA. MEROPS; InterPro; 3; Pkv.
pho00395; GLA; 1.
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PS50070; KRINGLE\_1; 1.
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PPRO01314; Chymotrypsin.
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w	ú	ú	53.5	ú	w	ú	4	4	S	6	6	σ	63	64	65	65	65	65	66	72	72	73	73	73.5	78	78	78	80
7.	.7	7.	7.	7.	7.	7.	7.	7	æ	8	œ	ω.			ω.	ω.	ω.	ω.	·	9		7.	37.1	7.	9	9.	9.	
576	568	543	506	506	431	196	603	567	575	651	606	459	678	674	674	673	198	179	25	809	98	399	49	ω	4	607	w	461
10	10	10	10	10	10	10	10	10	10	10	10								11	13	13		σ		6	IJ	6	თ
09C9U4	Q9ASC3	Q9MB23	Q9SE23	Q9SPF0	Q94EY5	004284	Q9LPG7	Q8W4J2	Q94E17	Q8S2I8	Q9SJG9	Q9SE22	Q14393	Q63772	Q99K57	Q61592	Q8R182	Q8TAS3	09QVH6	Q9PTW7	P82807	Q9CQW3	Q95ME8	Q90YK1	Q29094	Q91001	Q28994	Q95ND6
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## ALIGNMENTS

PRELIMINARY;

PRT;

456

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Created)
Last sequence update)
Last annotation update)

Canis Euteleostomi;

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SEQUENCE FROM N.A.
Leeb T., Kopp T., Deppe A., Breen
Brenig B.;
"Molecular characterization and cl
protein C gene.";
Mamm. Genome 10:135-139(1999).
                                                          InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR002383; GLA_blood.
                                                                                                                                                                                                                                                    Leeb T., Pfeiffer I., Kopp T., Deppe A., Brenig-B.; Analysis of canine protein C gene polymorphisms."; Analysis of canine protein C gene polymorphisms."; "In Genet. 30:237-238(1999).
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSTRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutheria; Carnivora; Fissipedia; Canidae;
NCBI_TaxID-9615;
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=99371952; PubMed=10443005;
                                             InterPró;
                                                                                                                                                                                       MEROPS;
                                                                                                                                                                                                        EMBL; AJ001979; CAA05126.1; HSSP; P04070; 1PCU.
                                                                                                                                                                                     S01.218;
IPRO02383; GLA_DIOUG.
IPRO01254; Ser_protease_Try.
TERO01254; V1tK_dep_GLA.
                                                                                                                                                                                                                                                                            PEPTIDASE FAMILY S1; ALSO KNOWN
                                                                                                                                                                                                                                 .'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Breen M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosomal assignment of the canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brunnberg
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Best Local S
Matches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R SMART; SMOOLER; EGF; 2.

R SMART; SMOOLER; TLA; 1.

R SMART; SMOOLER; Tryp_SPe; 1.

R PROSITE; SMOOLER; ASX_HYDROXYL; 1.

PROSITE; PSOOLER; EGF_1; UNKNOWN_1.

R PROSITE; PSOULER; EGF_2; 2.

R PROSITE; PSOULER; EGF_2; 2.

R PROSITE; PSOULER; EGF_CA; 1.

R PROSITE; PSOULER; EGF_CA; 1.

R PROSITE; PSOULER; TRYPSIN_DOM; 1.

R PROSITE; PSOULER; TRYPSIN_HIS; UNKNOWN_1.

R PROSITE; PSOULE; TRYPSIN_SER; 1.

R PROSITE; PSOULE; TRYPSIN_SER; 1.
Query Match
Best Local Similarity
                                                                                                                                                 Pfam; PF00008; EGF; 2.
Pfam; PF000594; gla; 1.
Pfam; PF00089; trypsin; 1
PROSITE; PS00010; ASX HYD
PROSITE; PS00022; EGF_1;
                                                                                           PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                         SEQUENCE
                                                                                                                                                                                                                                                                                      EMBL; BC013896; AAH13896.1; MGD; MGI:97771; Proc.
                                                                                                                                                                                                                                                                                                              Strausberg R.; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                             InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             091WN8
                                                                                                                                                                                                                    InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similar to protein C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydroxylation; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00722; CHYMOTRYPSIN PRINTS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                          InterPro; IPR0001
                                                                                                                                                                                                                                                                                                                                               CISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANSFLEEIRAGSLERECMEEICDFEEAKEIFQNVDDTLAYWSKY 86
                                                       lase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00594;
                                                                   PS00134;
PS00135;
                                                                                              PS00022; EGF_1; UNKNOWN_1.
PS01186; EGF_2; UNKNOWN_2.
PS01187; EGF_0A; UNKNOWN_1.
PS000011; GLU_CARBOXYLATION; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                         460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193
195
456 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gla; 1.
trypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat;
                                                                 TRYPSIN_DOM; 1; TRYPSIN_HIS; U
                                                     protease
                                                                                                                                                              ASX_HYDROXYL; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 P
194 P
456 P
50813 MW;
                                         51818 MW;
 71.1%;
59.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.6%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serine protease;
POTENTIAL.
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19,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Score 140; DB 11;
Pred. No. 1.3e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 151;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN C LIGHT CHAIN.
PROTEIN C CONNECTING DIPEPTIDE.
PROTEIN C HEAVY CHAIN.
7ADJA8C1C34E59FF CRC64;
                                                                 ; UNKNOWN_1.
; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                       0117F26E68FCC274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          460 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6;
1.6e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                 databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 456;
         Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                 RESULT
Q99PC6
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                                               Query Match
Best Local S
Matches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                            PROSITE; PS00135; TRYPSIN_SER; 1.
Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
Hydroxylation; Repeat; Serine protease.
SEQUENCE 460 AA; 51784 MW; 0293BC25E9D3ED16 CRC64;
                                                                                                                                                                 PROSITE; PROSITE;
                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Mus musculus (Mouse).
'arvota; Metazoa; Chordata;
'arta; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q99PC6
Q99PC6;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                           PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                          SMART; SM00001; EGF_lil
SMART; SM00069; GLA; 1
SMART; SM00020; Tryp_SI
                                                                                                                                                                                                                                                                      PRINTS; PR00722; CHYMOTRYPSIN. PRINTS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                                                         Pfam; PF00594; gla;
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF318182; AAK
HSSP; P04070; 1PCU.
                                                                                                                                                                                                                                                              SMART; SM0018
                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete sequence of UC72A01.";
Submitted (NOV-2000) to the EMBL/GenE
-i-SIMILARITY: BELONGS TO PEPTIDASE
TRYPSIN FAMILY.
                                                                                                                                                                                                                PROSITE; PS00010;
                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anticoagulant protein C.
                                                                                                                                                                                                                                                                                                                                            [nterPro;
                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:97771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                         nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                    nterPro;
42
                        1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
||||| :| ||| ||: ||:||:||:|||||| ||:
| 2 ANSFLEEMRPGSLERECMEBICDFBEAQEIFQNVEDTLAFWIKY
                                                                                                                                                                                                                                                                                             PF00089;
                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
                                                                                                                                                                                        PS00022;
PS01186;
                                                                                                                                                                  PS0001
                                                                                                                                                                                                                                                                                                                              IPR001254; Ser_protease_Try.
IPR000294; VitK_dep_GLA.
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                              0; Tryp_SPc; 1.
010; ASX_HYDROXYL; 1.
020; EGF_1; UNKNOWN_1.
186; EGF_2; 2.
187; EGF_CA; 1.
011; GLU_CARBOXYLATION; 1.
                                                                                                                                                                                                                                              1; EGF; 2.
1; EGF_like; 2.
                                                                                                                                                                                                                                                                                               trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK07918.1; -.
                                                                                                                                                                                                                                                                                                                                                                            152; Asx_hydroxyl.
314; Chymotrypsin.
561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                     3; GLA_blood.
                                                           68.0%;
56.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                               Score 134; DB 11;
Pred. No. 1.4e-14;
7; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     460
                                                                     DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      databases.
l; ALSO KNOWN
                                                                     Length 460;
  85
                        44
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AS
                                                0,;
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                                               Gaps
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                                               0;
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RESULT 4 Q63207

ΑC

Q63207 Q63207;

PRELIMINARY;

PRT;

482

AA.

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RESULT
054740
ID 056
AC 055
AC 057
DT 011
DT 011
DT 020
CC GN F1
OC F1
OC M:
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                                                                                                                                                                                                    Matches
                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                      PRINTS; PRO0722; CHYMOTYPSIN.

PRINTS; PRO0701; GLABLOOD.

SMART; SM00179; EGF_CA; 1.

SMART; SM00001; EGF_Ike; 1.

SMART; SM00001; Tryp_SPc; 1.

SMART; SM00001; ASX_HYDROXYL; 1.

PROSITE; PS00010; ASX_HYDROXYL; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS00134; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.

PROSITE; PS00135; TRYPSIN_SER; 1.
                                        054740 F
054740;
01-JUN-1998 (
01-JUN-1998 (
01-JUN-2002 (
Coagulation f
F10 OR FA10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001881; InterPro; IPR002383; InterPro; IPR001254; InterPro; IPR000294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (
01-NOV-1996 (
01-MAR-2002 (
Factor X.
Mus musculus (Mouse).
Plasmid pBluescript.
Eukaryote; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                          Calcium-binding;
Hydroxylation; Re
SEQUENCE 482 AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-SPRAGUE DAWLEY;
MEDLINE-96093366; PubMed-8578539;
Stanton C., Ross R.P., Hutson S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor-
Mammalia; Eutheria; Rode
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carboxylase., Thromb. Res. 80:63-73(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Evidence for competition
                                                                                                                           G
                                                                                                                                                           41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRYPSIN FAMILY
                                                                                                                                                        ANSFFEEIKKGNLERECVEEICSFEEAREVFEDNEKTTEFWNKY
                                                                                                                                                                            ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X79807; CAA56202.1;
P00742; 1XKA.
                                                                                                                                                                                                                                                                                                                                                                                                                       PF00089;
                                                                                                                                                                                                                                                                                                                                                                                                                      PF00594; gla; 1.
PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S01.216:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                 (TrEMBLrel. 06, Created)
(TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
factor x precursor (EC 3.4.21.6)
                                                                                                                                                                                                   Conservative
                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                     Repeat;
                                                                                                                                                                                                                                                            ; TRYPSIN_SER; 1. EGF-11ke domain; Glycoprotein; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; EGF_Ca.
; GLA_blood.
; Ser_protease_Try.
; VitK_dep_GLA.
                                                                                                                                                                                                                                            54265
                                                                                                                                                                                                           58.48;
                                                                                                                                                                                                                                           Serine protease.
265 MW; 0284678E3954A698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequ
Last anno
                                                                                                                                                                                                           Score 115;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                       PRT;
                                                                                                                                                                                                                                                                                   UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wallin R.;
vitamin K-
he vitamin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAMILY
                                                                                                      481
                                                                                                                                                                                                DB 11;
2.8e-11;
nes 15;
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K-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S1;
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 Muridae;
                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALSO
                                                                                                                                                                                                                     Length 482;
                                                                                                                                                          84
                                                                                                                                                                             44
                                                                                                                                                                                                   Indels
          Euteleostomi;
  Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AS
                                                                                                                                                                                                   0,
  Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factors
                                                                                                                                                                                                Gaps
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RESULT
Q99L32
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00065; GLX; 1.

SMART; SM00020; Tryp_SPc; 1.

SMART; SM00020; Tryp_SPc; 1.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS00022; EGF_1; UNKNOWN_1.

PROSITE; PS01186; EGF_2; 2.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS00011; GLU_CARBOXYLATION; 1.

PROSITE; PS00134; TRYPSIN_LDOM; 1.

PROSITE; PS00134; TRYPSIN_LSER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

Calcium-binding; EGF-11ke domain; Glycoprotein; Hy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00594; gla; 1.
Pfam; PF00089; trypsin; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PF00722; CHYMOTRYPSIN.
PRINTS; PF00001; GLABLOOD.
SMART; SM00179; EGF_CA; 1.
SMART; SM00001; EGF_like; 1.
                                                                                                                                                                                                                                            Q99L32
Q99L32;
01-JUN-2001
01-JUN-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000152; InterPro; IPR001314; InterPro; IPR000561; InterPro; IPR000742; InterPro; IPR001881; INTERPRO; I
Strausberg R.;
Submitted (FEB-2001) to
-i- SIMILARITY: BELONGS
TRYPSIN FAMILY.
                                                                                                                                       Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98454993; PubMed-9783672;
Heidtmann H.H., Kontermann R.E.;
"Cloning and recombinant express1
Thromb. Res. 92:33-41(1998).
                                                                                                                                                                                                                         Coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat; Serine
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ222677;
HSSP; P00742; 1
                                                                           SEQUENCE FROM N.A.
                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:103107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! - SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                                                                                  41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRYPSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                  ANSFFEEFKKGNLERECMEEICSYEEVREIFEDDEKTKEYWTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00008; EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P00742; 1XKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S01.216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and recombinant expression Res. 92:33-41(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR000294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001254;
                                                                                                                                                                                                                       (TrEMBLrel. 1 (TrEMBLrel. 1 factor X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481 AA;
                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                     (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protease; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAA10933.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 P
481 C
; 53986 MW;
                                                                                                                                              Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLA_blood.
Ser_protease_Try.
VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chymotrypsin.
EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Asx_hydroxyl
                           TO F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                      embt/GenBank/DDBJ databases PEPTIDASE FAMILY S1; ALSO KN
                                                                                                                                                                                                                                            Created)
Last sequence
Last annument
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 101; DB Pred. No. 7.4e 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
COAGULATION FACTOR
CF702DE5EF9D97AE
                                                                                                                                            Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                              sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of mouse coagulation factor X.";
                                                                                                                                                                                                                                                                                                                               481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                            on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                   Euteleostomi;
                           KNOWN
                                                                                                                                              Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid;
                           AS
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Best Local
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SMART; SM00011; EGF; 2.

SMART; SM00001; GLA; 1.

SMART; SM00002; Tryp_SPc; 1.

SMART; SM000020; Tryp_SPc; 1.

PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.

PROSITE; PS0001022; EGF_1; UNKNOWN_1.

PROSITE; PS01186; EGF_2; 2.

PROSITE; PS01187; EGF_2; 2.

PROSITE; PS00114; FRYPSIN_DOM; 1.

PROSITE; PS00114; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
STRAIN-129SJ;
Cooper A., Liang Z., Castellino F
Coloning and Characterization of
Thromb. Haemost. 0:0-0(2000).
-i- SIMILARITY: BELONGS TO PEPTID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                  Liang Z., Cooper A., DeFord M.E., Carmeliet P., Castellino F.J., Rosen E.D.;
                                                                                                                                                                                                                                                          STRAIN=C57BL6 X CBA; TISSUE=LIVER;
MEDLINE=98347933; PubMed=9684791;
                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                     F10.
                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                         Thromb.
                                                                                                                                                                           "Cloning and characterization of
factor X.";
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            088947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00135; TRYPSIN_SER; 1. Calcium-binding; EGF-like domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00594; gla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; S01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANSFFEEFKKGNLERECMEEICSYEEVREIFEDDEKTKEYWTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00089; trypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BC003877;
P00742; 1x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PR00722; CHYMOTRYPSIN
                                                                                                                                                       Haemost.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR000152; Asx_hydroxyl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001314; Chymotrypsin.
IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 08, Created)
(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; EGFBLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1XKA
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                                                                                                                                                     80:87-91(1998)
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                                         Castellino F.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGF_II.
GLA_blood.
      PEPTIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 101; DB 11;
Pred. No. 7.4e-09;
                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BD88E96C8A0B7E7F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                 b
                                                                                                                                                                                                 CDNA
                                              , Rosen
Murine
      FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481
                                                                                                                                                                                            encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                              E.D.;
Factor
    S1; ALSO KNOWN
                                                                                                                                                                                                                                        Collen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase;
                                                                                                                                                                                               murine coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
                                              x Gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                        Ŭ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481;
    AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat;
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    THE
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Best Local S
Matches 17
                               InterPro;
InterPro;
                                                                                                                                                                                                                                                 Q96PQ8;
                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Cr
01-DEC-2001 (TrEMBLrel. 19, La
01-MAR-2002 (TrEMBLrel. 20, La
Factor VII active site mutant
                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                            EMBL;
                                                                                  "Targeting tissue factor on tumor vascular endothelial cells for immunotherapy in mouse models of prostatic cells for immunotherapy in mouse models of prostatic cells for immunotherapy in Matl. Acad. Sci. U.S.A. 98:12180-12185(2001).
                                                                                                                     Hu Z., Garen A.;
                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
           [nterPro;
                      InterPro;
                                                     InterPro;
                                                               InterPro;
                                                                                                                              MEDLINE=21477448;
                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                Calcium-binding; EGF-lik
Serine protease; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00179; EGF_CA; 1.
SMART; SM00001; EGF_like; 1.
SMART; SM00069; GLA; 1.
SMART; SM00020; Tryp_SPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00722; CHYMOTRYPSIN. PRINTS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:103107; F10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF087644; EMBL; AF211347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; S01
                                                                                                                                          EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                41 ANSFFEEFKKGNLERECMEEICSYEEVREIFEDDEKTKEYWTKY
                                                                                                                                                                                                                                                                                                                                   1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRYPSIN FAMILY
                                                                           AF272774; AAK58686.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF087644;
                                                                                                                                                                                                                                                                                                                                                        l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00134;
                                IPR001881;
                                           IPR000742;
  IPR000294;
                                                     IPR000561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001881; EGF_Ca.
IPR002383; GLA_blood.
IPR001254; Ser_protease_Try.
IPR000294; V1tK_dep_GLA.
                       IPR003006;
                                                               IPR000152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR000152; Asx_hydroxyl.
IPR001314; Chymotrypsin.
IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                  481 AA;
                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ); Tryp_SPc; 1.
10; ASX_HYDROXYL; UNKNOWN_1.
102; EGF_1; UNKNOWN_1.
10; EGF_2; 2.
10; EGF_2; 2.
10; EGF_CA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1XKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          trypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC36345.1;
AAF22980.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                          FGF-like domain; Glycoprotein;
                                                                                                                               PubMed=11593034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRYPSIN_DOM; 1.
TRYPSIN_HIS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLU_CARBOXYLATION; 1.
        ; Asx_hydroxyl.
; EGF-like.
; EGF_2,
; EGF_Ca,
; Ig_MHC.
; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                        40
                                                                                                                                                                                                                                                                                                                                                                 51.3%;
38.6%;
                                                                                                                                                                                                                                                                                                                                                                                                  54018 MW;
VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                  Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                 Score 101;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                  COAGULATION FACTOR 8AC09DE5EF9D271E
                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                        Craniata; V
Catarrhini;
                                                                                                                                                                                                       immunoconjugate.
                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                            701
                                                                                                                                                                                    Vertebrata;
                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                                                                                                                                   .4e-09;
                                                                                                                                                                                                                                                                                                                                                                             DB 11; Length
                                                                                                                                                                         Hominidae;
                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase; Repeat;
                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                                                                                                                                                                                                   44
                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                   Euteleostomi;
                                                                                                          cells
                                                                                                                                                                                                                                                                                                                                                                              481;
                                                                                                         and
                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                          tumor
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0;

PF00008; EGF; PF00594; gla;

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PRESULTION OF REAL PROPERTY OF STREET OF STREE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                           Pfam; PF00594; gla; 1.
Pfam; PF00089; tryps1n; 1.
PRINTS; PR0072; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
SMART; SM00181; EGF; 2.
SMART; SM001079; EGF_CA; 1.
SMART; SM00001; EGF_L1ke; 2.
SMART; SM000069; GLA; 1.
SMART; SM000020; Tryp_SPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00022; E
PROSITE; PS01186; E
PROSITE; PS01197; E
PROSITE; PS00011; G
PROSITE; PS00290; IT
PROSITE; PS00240; T
PROSITE; PS00134; T
PROSITE; PS00135; T
                       PROSITE; PS00010; i
PROSITE; PS00022; i
PROSITE; PS01186; i
PROSITE; PS01187; i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21015017; PubMed=11132153; Poorafshar M., Aveskogh M., Munday B., Hellman L.; Poorafshar M., and structural analysis of four serine monotrome, the platypus, Ornithorhynchus anatinus."; Immunogenetics 52:19-28(2000).
                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ornithorhynchus anatinus (Duckbill platypus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF275654; AAG00453.1; HSSP; P00742; 1XKB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coagulation factor X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9GMD9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000294;
                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; S01.216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFW 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRYPSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANAFLEELRPGSLERECKEEQCSFEEAREIFKDAERTKLFW 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00089; trypsin; 1. ; SM00181; EGF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity 48.0
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            701 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                      Tryp_SPc; 1.
0; ASX_HYDROXYL; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRYPSIN_SER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASX_HYDROXYL; UNKNOWN_1.
EGF_1; UNKNOWN_1.
EGF_2; UNKNOWN_1.
EGF_CA; UNKNOWN_1.
EGF_CA; UNKNOWN_1.
  GLU_CARBOXYLATION;
                                          EGF_1; UNKNOWN_1.
EGF_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chymotrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77826 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.3%;
                                                                                                                                                                                                                                                                                                                                  Ser_protease_Try.
V1tK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                   EGF_Ca.
GLA_blood
                                                                                                                                                                                                                                                                                                                                                                                                                               EGF_2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEPTIDASE
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Pred. No. 2.5e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94AC6CEB42CC992F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAMILY S1; ALSO KNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; 1
2.5e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΑS
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RESULT
Q16519
ID Q1
AC Q1
DT 01
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Q9NSD0
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                                                                                                     Query Match
Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                           CHAIN
SEQUENCE
                                                                                                                                                             Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50240; TRYPSIN_DOM; PROSITE; PS00134; TRYPSIN_HIS; PROSITE; PS00135; TRYPSIN_SER; Hydrolase; Serine protease. SEQUENCE 469 AA; 52196 MW;
                                                                                                                                                                               Calcium-binding;
                                                                                                                                                                                                 PROSITE; PS00010; ASX_HYDROXYL; 3.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS01186; EGF_2; 3.
PROSITE; PS01187; EGF_CA; 2.
                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                         SMART; SM00282;
                                                                                                                                                                                                                                                 SMART;
                                                                                                                                                                                                                                                           SMART;
                                                                                                                                                                                                                                                                    PRINTS; PR00001;
                                                                                                                                                                                                                                                                           Pfam; PF00594; gla; 1.
Pfam; PF00054; laminin_G; 1.
                                                                                                                                                                                                                                                                                               Pfam; PF00008; EGF;
                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                 EMBL; X12892; CAA3
HSSP; P00740; 1CFH
                                                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                            Wydro R., Cc
Dahlback B.;
                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-LIVER
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9NSDO;
01-OCT-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9NSD0
                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                    11
                                                                                                                                                                                                                                                                                                                                                                                                                        EQUENCE FROM N.A.
                                                                 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41
                                                                           1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANSLFEELKKGNLERECNEETCSYEEAREVFEDTDKTNEFWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWS
                                                                 ANSLLEETKQGNLERECIEELCNKEEAREVFENDPETDYFYPKY
                                                                                                                                                                                                                                                ; PR00001; GLABLOOD.
SM00179; EGF_CA; 3.
SM00069; GLA; 1.
                                                                                                     17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Conserv
                                                                                                                                                                                                                                                                                                          IPR000294;
                                                                                                                                                                                                                                                                                                                     IPR0017
                                                                                                                                                                                                                                                                                                                                                                                                     Cohen E.,
                                                                                                                                                                                                                                                                                                                                                                                   (FEB-1992)
                                                                                                                                           650 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                     16
                                                                                                                                                                                                                                                                                                                                                                          CAA31383.1;
                                                                                                                                                                                                                                        LamG;
                                                                                                                        15
650
72480 MW;
                                                                                                                                                                               ; GLU_CARBOXYLATION; 1.
EGF-like domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                Asx_hydroxyl.
EGF-like.
EGF_Ca.
GLA_blood.
Laminin_G.
                                                                                                                                                                                                                                                                                                                                                                                                    Dackowski W., Stenflo J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.2%;
                                                                                                              43.1%;
                                                                                                                                                                                                                                                                                                         VitK_dep_GLA
                                                                                                                                                                                                                                                                                                                                                                          to the EMBL/GenBank/DDBJ
33.1; -.
                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                    Score 85; DB 4;
Pred. No. 6.1e-06.
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 95;
Pred. No.
                                                                                                                                          POTENTIAL. ; C67345ECE8645174 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 7.9e
7; Mismatches
                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4C66C230D0758F6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6;
7.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                     Lundwall
                                                                                                                     Length 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 469;
                                                                                                                                                                               Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42
                                                                                  44
                                                                                                     Indels
                                                                 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                     0
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                                                                                                                                                                                Repeat
                                                                                                     Gaps
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Q16519; Q16519; Q1-NOV-1996

(TrEMBLrel. 01, PRELIMINARY;

Created)

PRT;

650

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В
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Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00594; gla; 1.
Pfam; PF00054; laminin_G; 1.
Pfam; PF00001; GLABLOOD.
SMART; SM00179; EGF_CA; 3.
SMART; SM00069; GLA; 1.
SMART; SM00282; LamG; 2.
                                                                                                                                                                                                                                                                                                              NON_TER
                                 SEQUENCE FROM N.A.
MEDLINE-87182874; PubMed=3471151;
MacGillivray R.T., Irwin D.M., Gu
                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
        "Recombinant genetic approaches to functional mapping Ann. N. Y. Acad. Sci. 485:73-79(1986).
EMBL; M33031; AAA60220 1.
                                                                                                                                 01-DEC-2001
                                                                                                                                          01-NOV-1996
                                                                                                                                                  Q15253;
01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                     Q15253
                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PROSITE;
                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
InterPro;
                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=86313649; PubMed=2944113;
Lundwall A., Dackowski W., Cohen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stenflo J., Wydro R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                        Calcium-binding; EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00008; EG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein S
                                                                                                                        hrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolation and sequence of the cDNA
                                                                                                                                                                                        12
                                                                                                                                                                                                                   16
                                                                                                                                                                                                                                   1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                  ANSLLEETKQGNLERECIEELCNKEEAREVFENDPETDYFYPKY
M33031; AAA60220.1; P00735; 2PF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P00740;
                                                                                                                                                                                                                                                       l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coagulation.";
tl. Acad. Sci.
                                                                                                                      precursor
                                                                                                                                                                                                                                                                                                                                                            PS01187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000152; Asx_hydroxyl.
IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               precursor
                                                                                                                                                                                                                                                                                            650 AA;
                                                                                                                               (TrEMBLrel.
                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                      16
                                                                                                                                                                                                                                                                                                              4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA60181.1;
                                                                                                                                                                                                                                                                                                                                                                    ASX_HYDROXYL; 3.
EGF_1; UNKNOWN_1.
EGF_2; 3.
                                                                                                                       (Fragment).
                                                                                                                                                                                                                                                                                                     650
                                                                                   Chordata;
Primates;
                                                                                                                                                                                                                                                                                          72462 MW;
                                                                                                                                                                                                                                                                                                              15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Fragment).
                                                                                                                                                                                                                                                               43.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLA_blood.
Laminin_G.
                                                                                                                                                                                                                                                                                                                                       CARBOXYLATION; 1. like domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01,
19,
                                                                                                                                01,
01,
19,
                                                                                                                                                                                                                                                      10;
                                                                                                                               Last sequence up
Last annotation
                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                               Score 85;
Pred. No.
                                                                                                                                                                                                                                                                                         POTENTIAL.
PROTEIN S.
9A8C044C503BF474 CRC64;
                                                                                 Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83:6716-6720(1986).
                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                        sequence update)
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                                                                                                                                                                                                                                                              6.1e-06;
                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human protein
                                                                                                                                                                    ß
                                                                                  Hominidae;
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                                                                                                                               update)
                                                                                                                                                                                                                                                      17;
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                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                        Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mahr
                                                                                                                                                                                                                                   44
                                                                                                                                                                                                                  59
                                                                                                                                                                                                                                                      Indels
                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                           of thrombin.";
                                                                                                                                                                                                                                                                         650;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regulator
                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                        Repeat;
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                                                                                                                                                                                                               RESULT
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Best Local S
Matches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                Q61109;
Q61109;
01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                                                                                    Wang C.-P., Stafford D.W.;
"Halocynthia roretzi gla-like protein partial submitted (APR-2002) to the EMBL/GenBank/DDBJ EMBL; AF466701; AAL74247.2; -
SEQUENCE 542 AA; 62090 MW; EB9BF13FE42B32F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
NON_TER
                                            MEDLINE=96276538; PubMed=8701412; Tdusogie E., Rosen E., Geng J.P.,
                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal SIGNAL
        Idusogie E., Rosen Castellino F.J.;
                                                                   TISSUE=LIVER;
                                                                         SEQUENCE FROM N.A.
                                                                                                                          Mus musculus (Mouse).
                                                                                                                                             Coagulation
                                                                                                                                                       01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                 Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata;
Stolidobranchia; Pyuridae; Halocynthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000294; VitK. Pfam; PF00594; gla; 1. PRINTS; PR00001; GLABLOOD SMART; SM00069; GLA; 1.
                           "Characterization
                                                                                              NCBI_TaxID=10090;
                                                                                                                                     F7 OR FVII.
                                                                                                                                                                                                                                                                                                                                                                                                                             Gla-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8T6I3
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8T6I3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                            SHFEETQQGNLERECYEELCSFEEAREVFETNIQDLNEFWAKY
                                                                                                                                                                                                                                                              SFLXXLRQGSLXRXCIXXICDFXXAKXIFE-DVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTFLEEVRKGNLERECVEETCSYEEAFEALESSTATDVFWAKY
                                                                                                                                                                                                                                                                                  l Similarity
15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00011; GLU_CARBOXYLATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR002383; GLA_blood.
IPR000294; VitK_dep_GLA
                                                                                                                                            5 (TrEMBLrel. 5 (TrEMBLrel. 1) 2 (TrEMBLrel. 1) factor VII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 AA;
                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100
                          of a cDNA encoding murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43
>100
100
                                                                                                       Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11302 MW;
                                                                                                                                                                                                                                                                                         41.98;
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36.4%;
                                                                                                                                                     01,
01,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                                        21,
21,
21,
        TO PEPTIDASE FAMILY
                   (1996)
                                                                                                                                                                                                                                                                                Score 82.5; E
Pred. No. 1.3e
l0; Mismatches
                                                                                                                                                     Last sequence update)
Last annotation updat
                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                       Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                       EB9BF13FE42B32FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FD0E5D0174E1F6FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                              Carmeliet
                                                                                                                                                                                                                                                                                         82.5;
No. 1
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                                                                                                                                                                                             446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             542
                                                                                                                                                                                                                                                                                         ; DB 5;
l.3e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
        s1;
                                                                                                                                                                                                                                                                                                                                                                                                             Ascidiacea;
                           coagulation factor
                                                                                                                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
                                                                                                                                                                                                                                                                                                                                         genomic DNA databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 100;
         ALSO
                                              Collen
                                                                                                                                                                                                                                                                                                                       CRC64;
                                                                                                                                                                                                                                                              44
                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                               Euteleostomi;
          KNOWN
                                              0
                                                                                                                                                                                                                                                                                                                                                  sequence.";
         ΑS
                                                                                                                                                                                                                                                                                  1.
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                           VII:";
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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MEROPS; S01.21 MGD; MGI:10932

U44795; P08709;

AAC52570.1;

InterPro;

InterPro;

Asx\_hydroxy1 Aldehyde\_dehydr

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RESULT
Q14316
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00594; gla; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00721; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
SMART; SM00179; EGF_CA; 1.
SMART; SM00001; EGF_Like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00010; A
PROSITE; PS00022; E
PROSITE; PS00022; E
PROSITE; PS01187; E
PROSITE; PS00011; G
PROSITE; PS50240; T
PROSITE; PS50240; T
                                                                    [2]
SEQUENCE OF 3-19 FROM N.A.
MEDLINE-88327116; PubMed-3416069;
MEDLINE-PA Bertina R.M., Ploos
                                                                                                                                                                                                              014316;
01.NOV-1996 (TrEMBLrel. 01, Created)
01.NOV-1996 (TrEMBLrel. 11, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
F9 (Coagulation factor IX (Plasma THROMBOPLASTIC component, christmas disease, HAEMOPHILIA B)) (Factor IX).
                                                                                                                                                              P9 OR FACTOR IX.

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

MCBI_TaxID-9806;
                                                                                                                                                                                                                                                                                                                                                                                                                                    serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART;
                   "The putative factor IX gene promoter Blood 72:1074-1076(1988).
-I- SIMILARITY: BELONGS TO PEPTIDASE FTRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                         Q14316
                                                                   Briet E.;
                                                                                                                      Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                    1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFW 41
                                                                                                                                                                                                                                                                                                                                                ANSLLEELWPGSLERECNEEQCSFEEAREIFKSPERTKQFW
AL033403; CAA21954.1;
X55008; CAB38245.2; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM00020;
                                                                                                                                                                                                                                                                                                                                                                                           18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00135;
                                                                                                                                                                                                                                                                                                                                                                                                                                       446 AA;
                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; TRYPSIN_HIS;
5; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tryp_SPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114; Chymotrypsin.
164; Crystallin.
161; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASX_HYDROXYL; UNKNOWN_1.
CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
EGF_1; UNKNOWN_1.
EGF_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRYPSIN_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLU_CARBOXYLATION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        50318 MW; 482FD09BEFDA6870 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     40.6%;
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VitK_dep_GLA.
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Pred. No. 2.9e;05;
3; Mismatches 20;
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Pred. No. 3e-05;
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                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
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                                                                                 SEQ ID NO 35
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TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
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TYPE: PRT
ORGANISM: Homo :
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                                      LENGTH: 44
TYPE: PRT
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ORGANISM: HOMO FEATURE:
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US-08-474-042-2
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NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid US-08-955-636-20
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Patent No. 6017882
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                                                                                                                                                                                                                                                                          APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/002001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/08/955,636A CURRENT FILING DATE: 1997-10-23 NUMBER OF SEQ ID NOS: 35
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                                                          FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
                                                                                                                                       LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
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TYPE: PRT
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LOCATION:
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97.7%;
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                                                                                                                                         ; NAME/KEY: MOD_RES ; LOATION: (0)...(0) ; COATION: (0)...(0) ; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid US-08-955-636-22
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US-08-955-636-19
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                                                                    Best Loc
Matches
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SEQ ID NO 22
LENGTH: 44
TYPE: PRT
                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/08/955,636A CURRENT FILING DATE: 1997-10-23
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                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT TITLE OF INVENTION: POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 09531/002001
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                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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TYPE: PRT
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                                                                                   Local
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Local Similarity 95.5%;
nes 42; Conservative
                                  1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
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5. 6017882
                                                                    . Similarity 95.1
42; Conservative
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95.5%;
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Pred. No. 8.9e-22;
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US-08-955-636-1

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Sequence 1, Application US/08955636A Patent No. 6017882

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: OTHER INFORMATION: Xea-gamma carboxyglutamic acid
US-08-955-636-1
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US-08-955-636-25
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Patent No. 6017882
                                                                                                                          Patent No. 5847085
GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FASTSEQ for Windows Version 3.0
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ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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                                                                                               APPLICANT: CHARLES TITLE OF INVENTION:
                                                                                NUMBER OF SEQUENCES:
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                               ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West
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Pred. No. 2e-20;
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Pred. No. 2e-20;
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US-08-295-411-1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Sequence 1, Application US/08295411 Patent No. 5679639
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                         GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/745,254
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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                                                                                                             NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
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MEDIUM TYPE: Floppy disk
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                                       ADUAL
STREET: La
COUNTRY: US
ZIP: 92037
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Pabst, Patrea L
REGISTRATION NUMBER: :
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                                                                                             Office of Patent Counsel, The Scripps
                                                                              Research Institute
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Rolf M.
                                                              5679639th Torrey Pines Road, TPC
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/note= "where Xaa means
carboxylglutamic acid"
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Pred. No. 2.1e-20;
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Therapeutic Methods
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LOCATION: Region 170..419

OTHER INFORMATION: //
US-08-295-411-1
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Best Local Similarity 70.5
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                                                                                                                                                                                                                                                                  ENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                               UMBER OF SEQUENCES:
                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                 ADDRESSEE:
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OPERATING SYSTEM:
                                                                      COUNTRY:
                                                                                                                   STREET:
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OPERATING SYSTEM:
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REFERENCE/DOCKET NUMBER: TSRI263.0C1
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                                                                                                                   10666 No.
                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419 amino acids
                                                                                                                                                                                                                                                  Griffin,
                                                                                                                                                                                                                                      Mesters,
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1..157
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                                                                                                                                           Office of Patent Counsel, The Scripps
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                                                                                                                             Research
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                                                                                                                                                                                                                                    John H.
Rolf M.
                                                                                                                                                                                      Serine Protease-Derived Polypeptides and Anti-Peptide Antibodies, Systems and Therapeutic Methods for Inhibiting Coagulation
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                                                                                                             5968751th Torrey Pines Road, TPC
                                                                                                                                                                                                                                                                                                                                                                                                                                         81.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Protein C Heavy Chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Protein C
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Pred. No. 2.7e-19;
2; Mismatches 11
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LOCATION: 170..419
COTHER INFORMATION: //
US-08-955-471-1
                                              ; ORGANISM: Homo sapiens US-09-667-570A-3
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US-09-667-570A-3
                                                                                                                    SEQ ID NO 3
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                    sequence 3, Application US/09667570A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 70.9
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/045,255 PRIOR FILING DATE: 1997-04-28 NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/667,570A CURRENT FILING DATE: 2000-09-21
                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                            APPLICANT: Sheliga, Theodore A
TITLE OF INVENTION: Improved Methods for Processing Activated Protein C
                                                                                                                                                                                                                                       FILE REFERENCE: X-11796A
                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                     APPLICANT: Baker,
                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE
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LOCATION: 158..169
OTHER INFORMATION: ,
OTHER INFORMATION: ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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REFERENCE/DOCKET NUMBER: TS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                        INFORMATION:
                                                                                                      419
                                                                                                                                    PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                      Huang, Lihua
                                                                                                                                                                                                                                                                                                       Carlson, Andrew D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          419 amino acids
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1..157
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                                                                                                                                                                                                                                                                                                                       Jeffrey C
 81.2%;
70.5%;
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Peptide"
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Score 160; DB 4;
Pred. No. 2.7e-19;
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Pred. No. 2.7e-19
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Matches

31;

Conservative

2;

Mismatches

11;

Indels

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0

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Matches
                                                            Query Match
Best Local Similarity
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
LENGTH: 419 amino acid
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                                                                                                                                                                               NAME/KEY: Region
LOCATION: 158..169
OTHER INFORMATION: OTHER INFORMATION: I
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COUNTRY:
92037
                                                                                                                    NAME/KEY: Region LOCATION: 170..419 OTHER INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polonia
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                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear LECULE TYPE: protein POTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PFILING DATE: 19921118
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1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                        OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                      NAME/KEY: Region
LOCATION: 1..157
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                                                                                                                                                                                                                                                                                                                   SENSE:
                                                                                                                                                                                                                                                                                                                                                                       AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                       419 amino acids
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                                              Conservative
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                                                          81.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serine Protease-Derived Pclypeptides Anti-Peptide Antibodies, Systems and for Inhibiting Coagulation
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                                                                                                                                                                             /note= "Protein C Activation
Peptide"
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                                                                                                                     /note= "Protein C Heavy Chain"
                                                                                                                                                                                                                                                        /note=
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                                                         Score 160; DB 5; pred. No. 2.7e-19;
                                                                                                                                                                                                                                                    "Protein C Light Chain
                                           Mismatches
                                                                        DB 5; 'Length 419;
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                                           Indels
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Therapeutic Methods
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                                                                                                                                                                       Sequence 4, Apr. 5905185
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 31; Conserv
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                                                                                                                                                              GENERAL
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                                                          ITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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                                                                                                                                                               INFORMATION:
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                             SEQUENCES:
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                                                                                                                                                 Garner,
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ymoGenetics, Inc
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; MOLECULE TYPE: protein US-08-756-506-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                    43 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                   1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKH 44
INVENTION: ANIMALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
                                                                                                                                                                            Application US/08756506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sawislak, Deborah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                460 amino acids
              Sprecher, Cindy A. Prunkard, Donna E. PROTEIN C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206-442-6678
                                                                                                    Cottingham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cottingham, Ian F
Temperley, Simon
Foster, Donald C.
                                                                                       Temperley, Simon M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sprecher, Cindy A. Prunkard, Donna E.
                                                                      Foster, Donald C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION
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                                                                                                      Ian R
                                                                                                                                                                                                                                                                                                                                                       Score 160; DB 2
Pred. No. 3.1e-1
                  PRODUCTION IN TRANSGENIC
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                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                        Length 460;
                                                                                                                                                                                                                                                                    86
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COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,506
FILING DATE:
APPLICATION NUMBER: 37.438
REGISTRATION NUMBER: 37.438
REGISTRATION NUMBER: 95-28
TELEPHONE: 206-442-6678
INFORMATION: 206-442-6678
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 460 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
Search completed: May 16, 2003, 10:16:12 Job time: 15 secs
                                                                                                                                        Query Match 81.2
Best Local Similarity 70.5
Matches 31; Conservative
                                                               STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
                                                                                                                                                         81.2%;
                                                                                                                                    Score 160; DB 2; Length 460; Pred. No. 3.1e-19; 2; Mismatches 11; Indels
                                                                                                                                    0; Gaps
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No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                          Score
160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362588 segs, 96450795 residues
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Published_Applications_AA: *
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/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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          US-10-182-263-1
US-09-978-917A-4
US-10-182-263-2
US-09-978-917A-2
US-10-107-122-2
US-10-109-498-1
US-09-759-130B-313
US-10-189-123-43
US-10-189-123-42
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US-10-182-263-3
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US-10-182-263-5
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77.161, Million cell updates/sec
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Compugen Ltd.
                         Sequence 2, Appli
Sequence 1, Appli
Sequence 313, Appl
Sequence 313, Appl
Sequence 42, Appl
Sequence 312, Appl
Sequence 310, Appl
Sequence 40, Appl
Sequence 40, Appl
Sequence 5, Appli
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Sequence
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3, Appli
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5, Appli
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4	4	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
4	44.5	45	47	47	47	47	47	47	47	47	47	47	47	47	47	48	48	48	49	64.5	64.5	64.5	64.5	64.5	64.5
22.5	22.6	22.8	23.9																	32.7	32.7	32.7	32.7	32.7	32.7
0	4 9	254	1367	1367	1367	1356	1356	1356	367	367	367	317	317	317	180	1363	1298	348	1363	225	225	208	208	95	95
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05-09-790-092-2179	US-09-836-392-34	US-09-796-149-4	US-09-872-136-6	US-09-766-678-2	US-09-919-408-6 '	US-10-100-405A-2	US-10-022-939-2	US-09-969-037-7	US-09-939-832-12	US-09-939-754-12	US-09-939-833-12	US-09-939-832-5	US-09-939-754-5	US-09-939-833-5	US-09-766-678-6	US-09-375-248-2	US-09-982-610-33	US-09-982-610-18	US-09-375-248-19	US-10-189-123-83	US-09-759-130B-353	US-10-189-123-85	US-09-759-130B-355	US-10-189-123-86	US-09-759-130B-356
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sequence zi/9, Ab	Sequence 34, Appl	(i)	Sequence 6, Appli	Sequence 2, Appli	Sequence 6, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 7, Appli	Sequence 12, Appl	Sequence 12, Appl	Sequence 12, Appl	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Seguence 6, Appli	Sequence 2, Appli	<ul> <li>Sequence 33, Appl</li> </ul>	Sequence 18, Appl			Sequence 353, App	Sequence 85, Appl	Sequence 355, App	70	Sequence 356, App

## ALIGNMENTS

RESULT 1 US-10-182-263-6

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В
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TYPE: PRT
ORGANISM: Homo sapiens
US-10-182-263-6
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US-10-182-263-3
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Sequence 3, Application US/10182263
Publication No. US20030022354A1
GEMERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/10182263
Publication No. US20030022354A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
                                                                                                                                                                                                                                                                                                                      Query Match 90.9
Best Local Similarity 79.9
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
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79.5%;
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Pred. No. 5.4e-22;
0; Mismatches 9
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; ORGANISM: Homo sapiens
US-10-182-263-4
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                                                                                                                                                                                                      Sequence 5, Application US/10182263 Publication No. US20030022354A1
                                                                                                                                                                                       GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO
                  FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
                                                                                                        APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
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                                                                                                                                                                APPLICANT: Gerlitz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.1
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CURRENT FILING DATE: 2002-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.1
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PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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77.3%;
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77.3%;
60/189199
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Pred. No. 3.8e-21;
0; Mismatches 10
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Pred. No. 3
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US-09-978-917A-4
                                                                    ; ORGANISM: Homo sapiens
US-09-978-917A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens US-10-182-263-1
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                    Query Match
Best Local
                                                                                                                                    SEQ ID NO 4
   Matches
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09978917A Publication No. US20030027299A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                       FILE REFERENCE: 0219us310 - protein C or activated protein C-like molecules CURRENT APPLICATION NUMBER: US/09/978,917A
CURRENT FILING DATE: 2001-10-17
NUMBER OF CENTRAL PROPERTY OF CENTRAL PROPERTY FILING DATE: 2001-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1
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Best Local Similarity 77.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO
                                                                                                                                                      SOFTWARE: PatentIn Ver.
                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                     LENGTH: 419
TYPE: PRT
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PRIOR FILING DATE: 2000-03-14
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CURRENT FILING DATE: 2002-07-22
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TYPE: PRT
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               Score 160; DB 9; Pred. No. 8.6e-19;
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Pred. No. 8.6e-19;
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No. 3.8e-21;
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RESULT 9
US-10-017-122-2
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US-09-978-917A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 0219us310 - protein C
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CURRENT FILING DATE: 2002-07-22
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                                                                                                                                                                                                                                                                                                         NAME/KEY: SIGNAL
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                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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TYPE: PRT
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les 31; Conserv
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Grinnell, Brian W
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Pred. No. 9.5e-19;
2; Mismatches 11
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Pred. No. 9.5e-19;
2; Mismatches 11
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US-09-759-130B-313

GENERAL INFORMATION:

Millennium Pharmaceuticals, McCarthy, Sean A

McCarthy, Seam A

APPLICANT APPLICANT

APPLICANT PPLICANT

Sharp,

John D

Thomas S

Kirst, Susan J Barnes, Sequence 313, Application US/09759130B Publication No. US20030022279A1

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CURRENT FILING DATE: 2001-12-14
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CURRENT FILING DATE: 2002-03-22
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TITLE OF INVENTION: Coagulation Factor VII Derivatives
FILE REFERENCE: 6286.200-US
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                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
                                                                                                                                                         NAME/KEY: VARIANT
LOCATION: (1)...(406)
OTHER INFORMATION: Xaa - Any Amino Acid
                                                                                                                                                                                                                                                   TYPE: PRT
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                                                                     Local Similarity
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ANAFLXXLRPGSLXRXCKXXQCSFXXARXIFKDAXRTKLFW 41
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70.78;
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; Pred. No. 5e-0
3; Mismatches
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; ORGANISM: Homo sapiens US-10-189-123-43
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                                                                                   SEQ ID NO 43
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Publication No. US20030082586A1
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                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/342,364 PRIOR FILING DATE: 1999-06-29
                                                                                                                                                                                                                                                                               APPLICANT: BARNES, Thomas S.
TITLE OF INVENTION: ANTIBODIES HAVING DIAGNOSTIC. PREVENTIVE, THERAPEUTIC, AND OTHER FILE REFERENCE: 10147-11U3
                                                                                                       SOFTWARE: PatentIn version 3.1
                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/596,194 PRIOR FILING DATE: 2000-06-16
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                                          LENGTH: 96
TYPE: PRT
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TYPE: PRT
ORGANISM: Homo sapiens
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FILING DATE: 2000-05-24
APPLICATION NUMBER: US 09/333,159
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FRASER, Christopher C.
SHARP, John D.
Thomas S.
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Best Local Similarity
Matches 17; Conserv
                                   Query Match
                                                                                                                                     SOFTWARE: Fa
                                                                                                                                                                         NUMBER OF SEQ ID NOS:
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CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 09/479,249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HOLTZMAN, DOUGLAS A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE,
TITLE OF INVENTION: USES
FILE REFERENCE: MP100-5350MNIM
                                                                                      TYPE: PRT
ORGANISM: Homo
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                                                                                                                    ENGTH:
 Local Similarity 38.0 hes 17; Conservative
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APPLICATION NUMBER: US 09/559,497

FILLING DATE: 2000-04-27

APPLICATION NUMBER: US 09/578,063
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                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2000-05-24
APPLICATION NUMBER: US 09/333,159
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                                                                                                                         209
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o. US20030022279A1
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              42.9%;
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                                                                                                                                                                                                                                                                                                                                           US 09/342,364
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Score 84.5; DB 9;
Pred. No. 2.1e-06;
B; Mismatches 18;
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Pred. No. 9e-07;

8; Mismatches
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RESULT 14 US-10-189-123-42 Sequence 42, Application US/10189123

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2 NSF-LXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

NRFDLELFTPGNLERECNEELCNYEEAREIFVDEDKTIAFWQEY

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US-10-189-123-42
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LENGTH: 209
TYPE: PRT
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APPLICANT: FRASER, Christopher C.
APPLICANT: SHARP, John D.
APPLICANT: BARNES, Thomas S.
TITLE OF INVENTION: ANTIBODIES HAVING DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER FILE REFERENCE: 10147-1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -09-759-130B-310
                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/759,130B CURRENT FILING DATE: 2002-09-16 PRIOR APPLICATION NUMBER: US 09/479,249 PRIOR FILING DATE: 2000-01-07 PRIOR APPLICATION NUMBER: US 09/559,497 PRIOR APPLICATION NUMBER: US 09/578,063 PRIOR FILING DATE: 2000-05-24
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NUMBER OF SEQ ID NOS: 100
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PRIOR APPLICATION NUMBER: US 09/596,194
PRIOR FILING DATE: 2000-06-16
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RPPLICANT: HOITEMAN, Douglas A
RITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
RITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
RITLE OF INVENTION: USES.
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les 17; Conservative
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                                                                                       APPLICATION NUMBER: US 09/342,364 FILING DATE: 1999-06-29 APPLICATION NUMBER: US 09/608,452
                                                                                                                                                                  APPLICATION NUMBER: US 09/333,159
FILING DATE: 1999-06-14
APPLICATION NUMBER: US 09/596,194
FILING DATE: 2000-07-14
                                                                     FILING DATE: 2000-06-30
                                            APPLICATION NUMBER: US 09/393,996
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Kirst, Susan J
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Wrighton, Nicolas
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Sharp, John D
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NUMBER: US 09/602,871
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Pred. No. 2.1e
8; Mismatches
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